

FIG. 1A

BHR (PC20 \leq 16 mg/ml) & Asthma

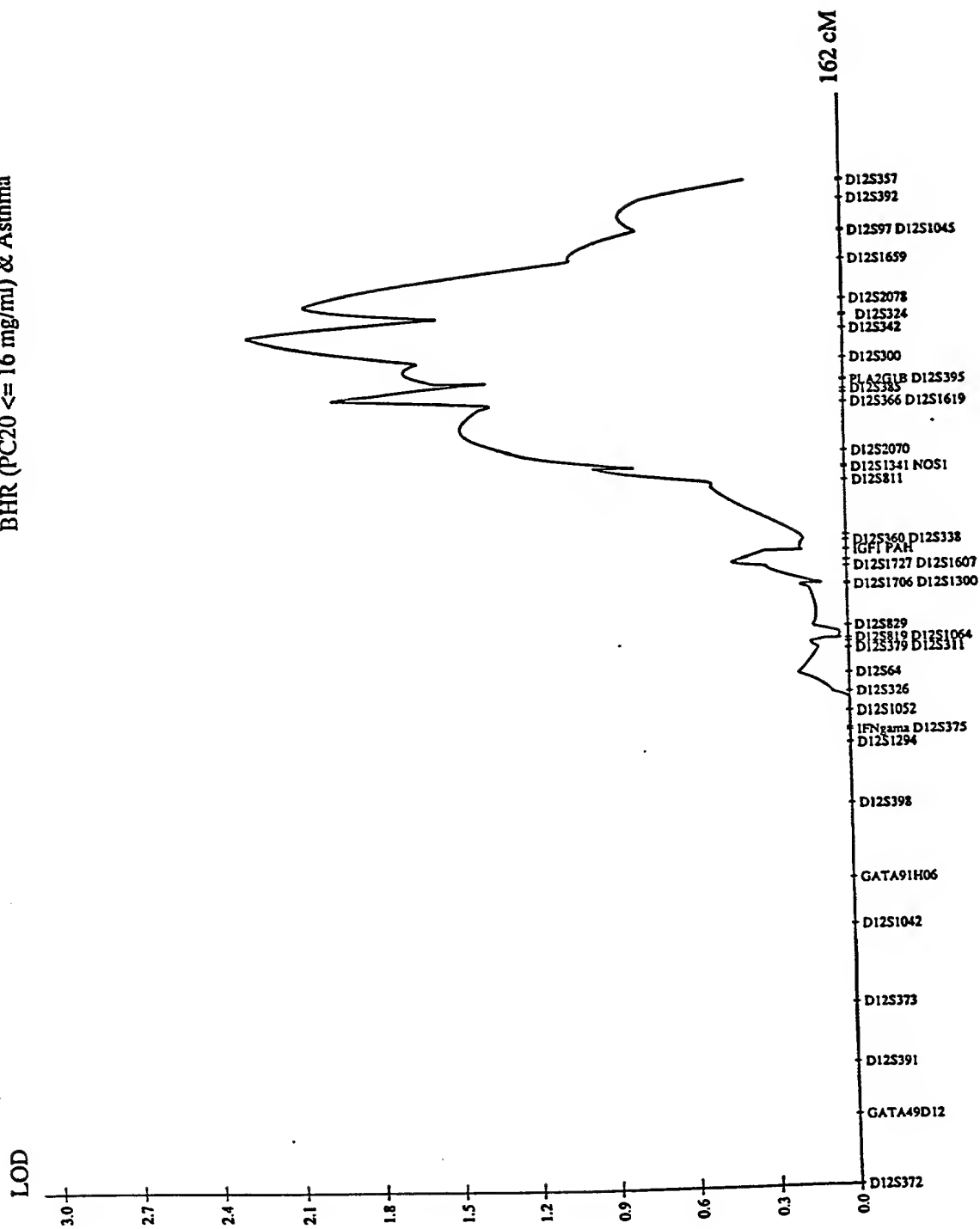


FIG. 1B

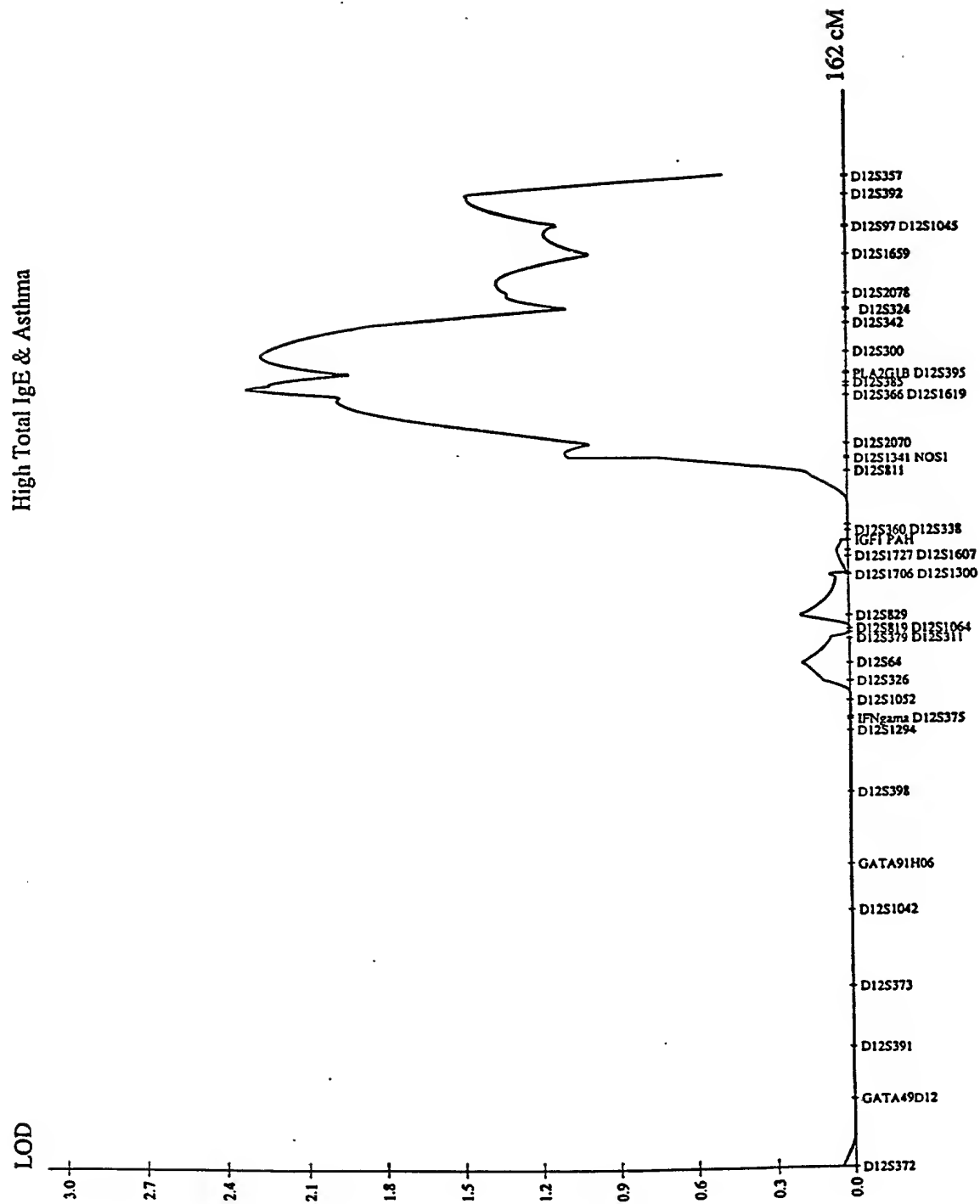


FIG. 1C

High Specific IgE & Asthma

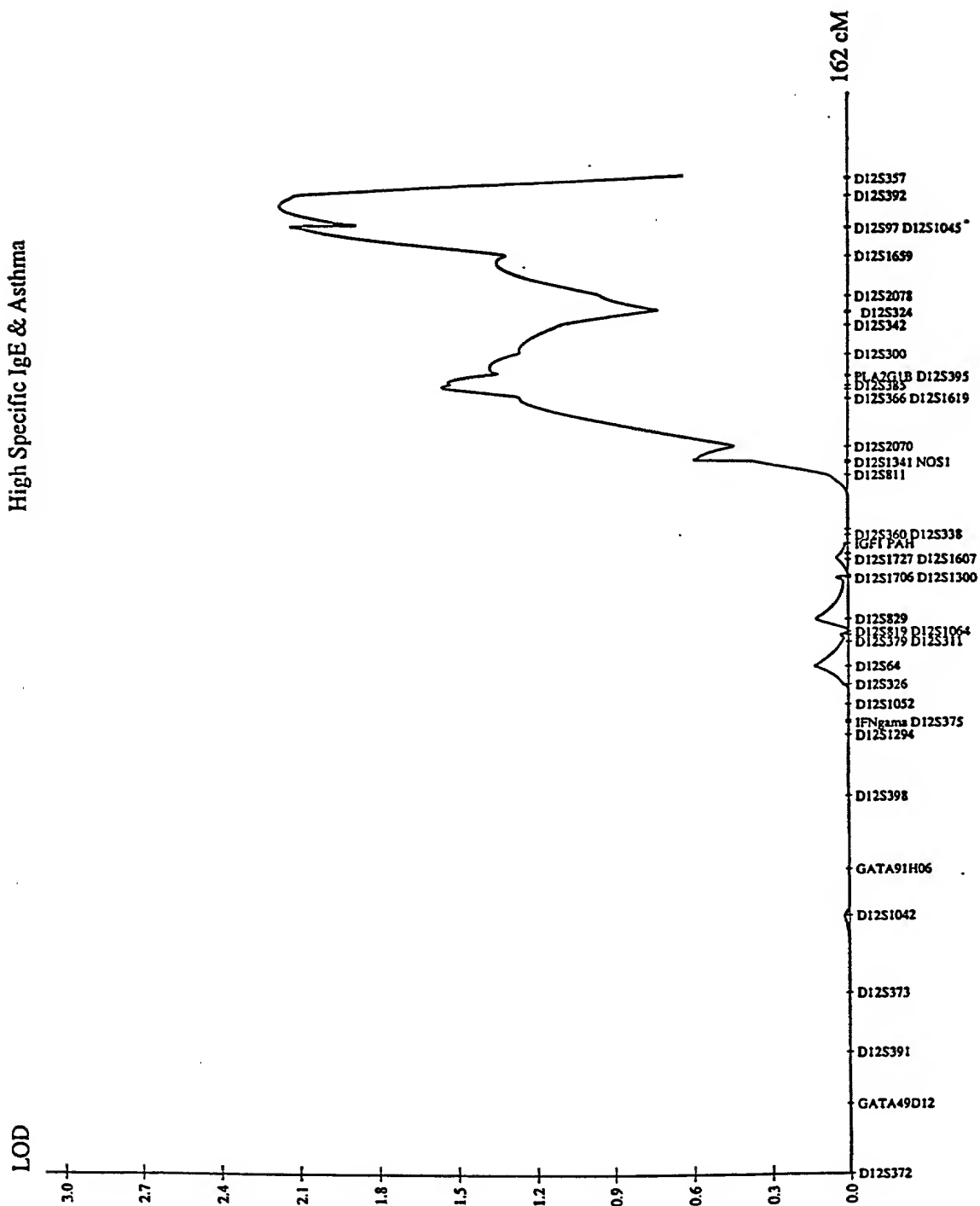
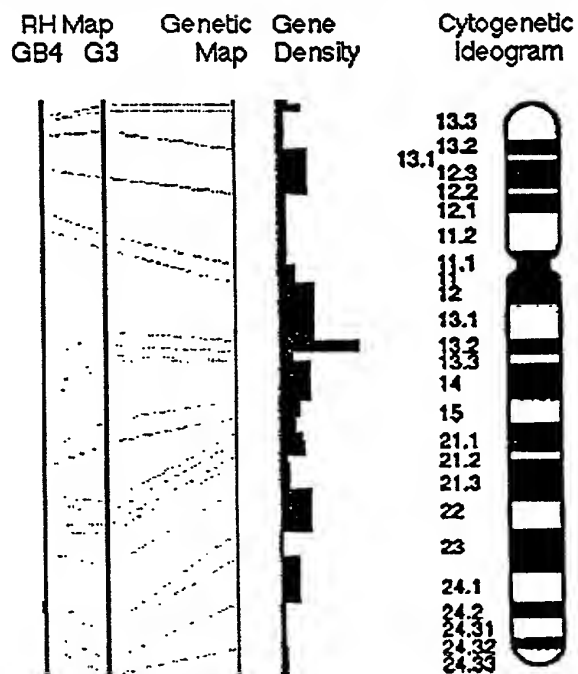


FIG. 1D

Chromosome 12: D12S79-D12S366



Error Flags

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy

The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S79 (126.1 cM)
 Bottom of interval: D12S366 (133.8 cM)
 Genetic size of bin: 8 cM
 Physical size of bin: 9 cR3000

FIG. 2 A

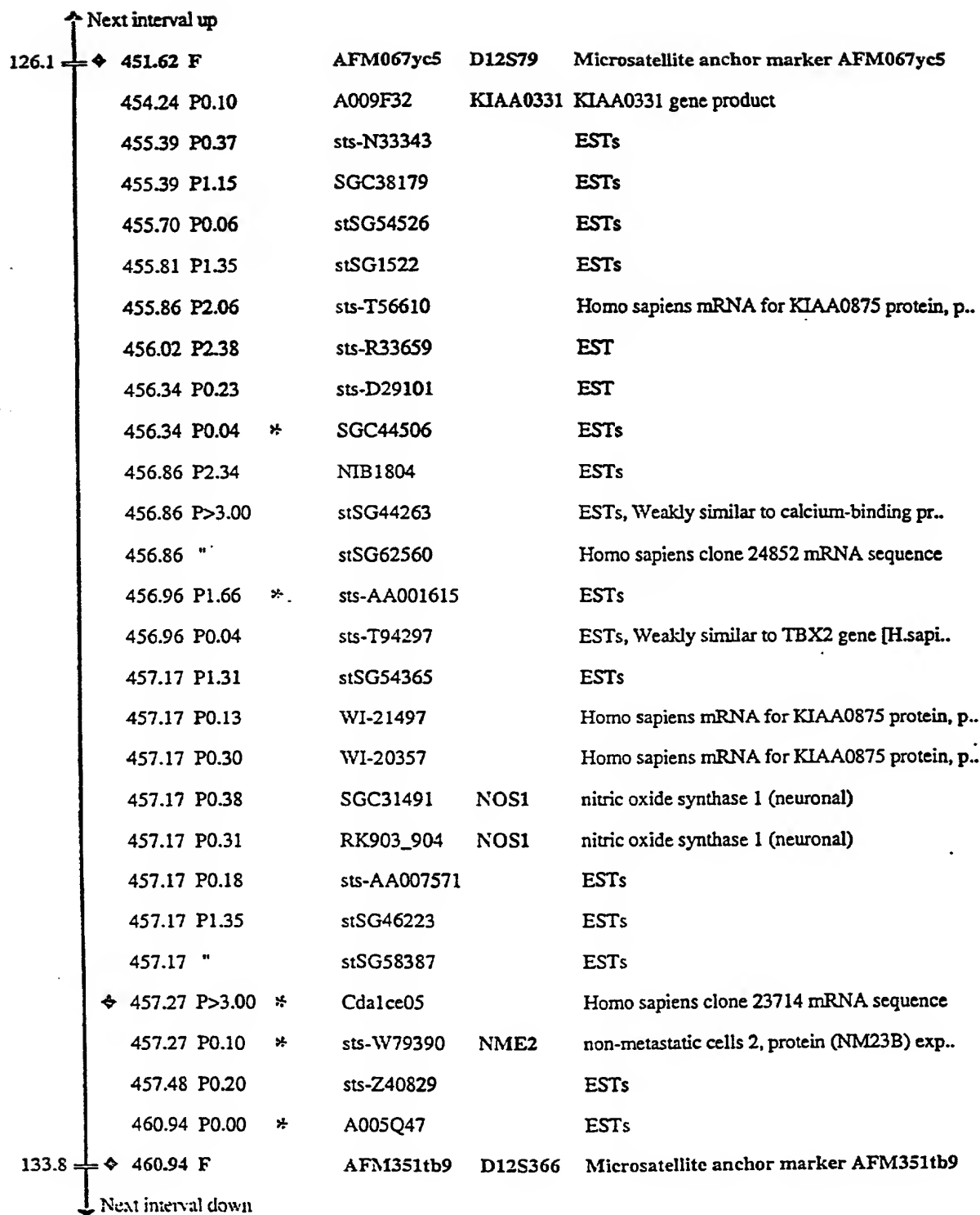
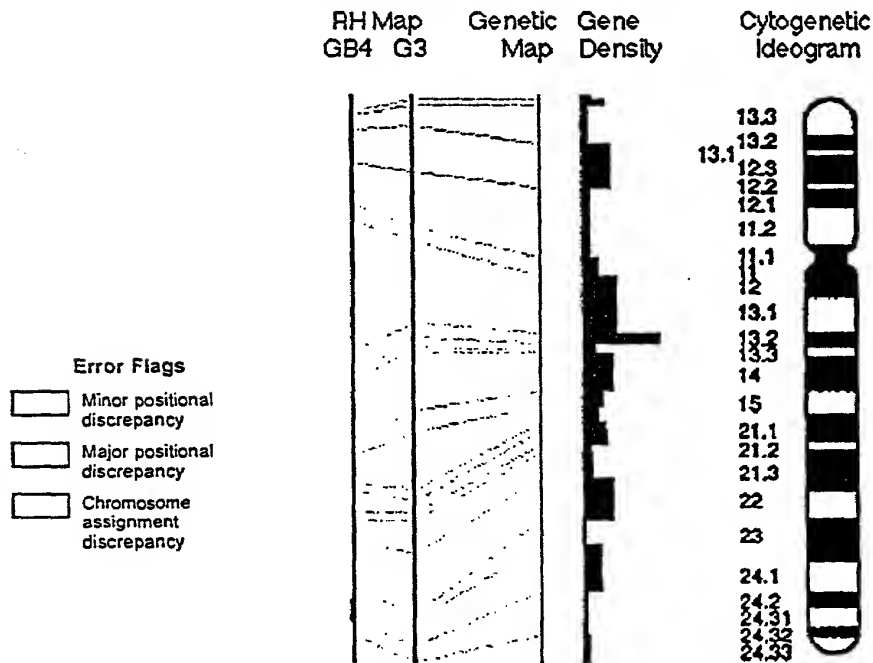


FIG. 2 B

Chromosome 12: D12S366-D12S340



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

Physical size of bin: 21 cR3000

133.8	Next interval up			
460.94	F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
462.85	P1.00	*	stSG8109	ESTs
462.85	"	sts-X75252	PBP	prostatic binding protein
462.95	P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2 C

463.77 P0.19	WI-16745		Human clone 37, 5cM region surrounding hepa..
◆ 463.77 P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98 P0.02	A008B04		ESTs
463.98 "	stSG50309		ESTs
463.98 "	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98 P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98 P0.08	R06295		EST
463.98 P1.33	sts-W56792		ESTs
464.08 P2.32	A007E48		ESTs
464.19 P1.28	A009U43		ESTs
464.29 P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39 P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39 P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39 "	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39 P1.09	stSG29626		ESTs
464.39 P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39 "	A001T32	PXN	paxillin
464.39 "	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39 "	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39 "	sts-T95105		ESTs
464.39 "	Cda0id01		ESTs
464.39 P1.13	stSG31431		ESTs, Moderately similar to (define not a..
◆ 464.39 " *	WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39 "	1B1092		Homo sapiens clone 23714 mRNA sequence
464.39 "	T79466		ESTs
464.39 P1.18	stSG48379		ESTs
464.45 P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45 "	stSG40392		ESTs
464.45 "	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49 P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49 P0.25	sts-AA002185	PXN	paxillin
464.49 P0.10	stSG48442		ESTs
464.49 "	sts-T16456		ESTs
464.49 "	stSG62260		ESTs

FIG. 2 D

	464.49	"	NIB1331		ESTs
	464.49	"	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49	"	WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
	464.49	"	SGC34758		ESTs
	464.49	"	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49	"	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49	"	SGC32343		ESTs
	464.79	P0.96	SGC33521		ESTs
	464.79	P0.96	* X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20	P0.20	sts-H10302		ESTs
◆	465.38	P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41	P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41	"	stSG22726		EST
	465.41	"	WI-17776		ESTs
	465.41	"	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41	"	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41	P0.77	stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
	465.41	"	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41	P0.80	stSG46660		EST
	465.51	P0.75	stSG41086	PXN	paxillin
	465.51	P0.83	stSG52121		ESTs
	465.91	P0.01	WI-16071		ESTs
	465.91	P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62	P0.00	sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
	466.71	P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91	P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91	P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01	P0.01	stSG52567		ESTs
135.1	467.11	F	AFM123xb2	D12S86	Microsatellite marker AFM123xb2
135.1	467.11	P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11	P0.01	AFM123xb2		Unknown
137.5	◆ 467.21	P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21	P0.02	sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
	467.21	P0.02	stSG8721		EST

FIG. 2 E

467.21	"	stSG44224		ESTs
467.21	"	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21	"	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21	"	stSG47820		ESTs
467.21	"	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21	"	stSG15021		ESTs
467.21	"	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆ 467.21	"	H50549	KIAA0262	KIAA0262 gene product
467.21	P0.03	SGC35167		EST
467.21	P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21	P0.02	WIAF-607		Unknown
467.31	P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93	P0.85	SGC31344		EST
469.13	P0.90	A007C39	A CADs	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13	P0.14	stSG35104		ESTs
469.13	"	A006Q41		Unknown
469.23	P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33	P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sapi..
469.33	"	R01708		EST
469.33	"	stSG54819	HCALB_BR	calbrain
469.33	"	A001Z45		ESTs, Highly similar to (define not avail..
469.33	"	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..
469.33	"	stSG63173		EST
469.33	"	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42	P1.01	WI-16068		EST
469.44	P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44	"	stSG62627		EST
469.44	"	stSG36007		Homo sapiens full length insert cDNA clone..
469.44	"	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44	"	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44	"	stSG62591		ESTs
◆ 469.54	P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62	P1.03	sts-N34573		ESTs
469.62	P1.03	sts-N58045		ESTs

FIG. 2 F

469.62	P1.04		WI-13224		EST	
469.83	P1.12		SGC34424		ESTs	
469.93	P1.14		stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..	
470.14	P1.17		stSG52516		ESTs, Weakly similar to (define not avail..	
470.24	P1.32		D0S1735E		ESTs	
470.24	P1.12		WI-6178		ESTs	
470.32	P1.25		sts-U29895		Unknown	
470.32	P1.24		WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..	
470.43	P1.29		stSG52094		ESTs	
470.63	P1.38		A004017		ESTs	
◆	470.77	P1.32	**	SGC33451	ESTs, Weakly similar to rhoHP1 [H.sapiens..	
◆	470.84	P1.35	**	sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
	470.84	P1.52		WI-13062		Homo sapiens mRNA, expressed in fibroblast..
	471.27	P1.60		sts-R99269		EST
	471.37	P1.70		stSG1991		ESTs
	471.37	"		stSG15859		Homo sapiens full length insert cDNA YQ02..
	471.58	P1.78		stSG29729		ESTs, Weakly similar to (define not avail..
	471.58	P1.37		WI-16979		ESTs
	471.65	P1.39		WI-17693		EST
	471.80	P1.29		WI-22060		ESTs
	471.90	P>3.00		stSG8210		ESTs, Moderately similar to neuronal threa..
	471.90	"		WI-17956		EST
	471.90	"		WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
	471.90	"		stSG47029		ESTs
	471.90	"		stSG47647		EST
	471.90	"		sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆	471.90	"	**	WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
	471.90	"		NIB962		ESTs
	471.90	"		A009E34		ESTs, Moderately similar to neuronal threa..
	471.90	"		sts-T17477		ESTs
	472.08	P1.49		sts-X89984		H.sapiens mRNA for BCL7A protein
	472.12	P>3.00		SGC34693		EST
	472.12	P>3.00		A009O01		ESTs, Weakly similar to neuronal thread pr..
	472.29	P>3.00		stSG47084		ESTs

FIG. 2 G

472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor; GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

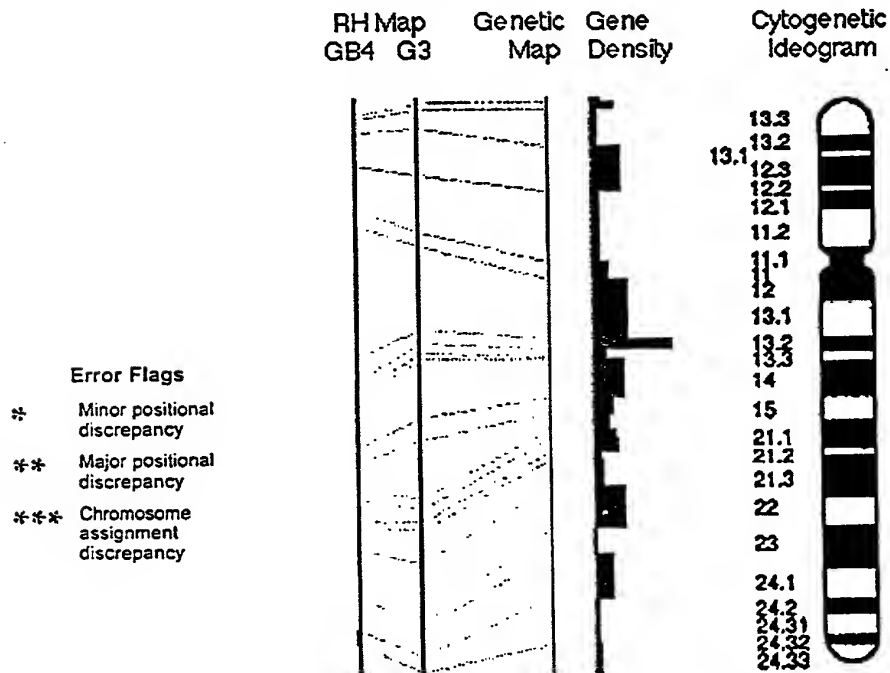
FIG. 2 H

	475.18 P>3.00	WI-22211		Homo sapiens full length insert cDNA clone..
	475.18 P2.08	stSG48093		ESTs
	475.18 "	A004P27		ESTs, Weakly similar to MULTIDRUG RESL..
	475.35 P2.10	stSG9904		ESTs
	475.40 P0.45	sts-AA024696		ESTs
	475.51 P>3.00	stSG53793		ESTs
	476.10 P>3.00	Bda98d05		Homo sapiens full length insert cDNA clone..
	476.21 P>3.00	sts-H24468		ESTs
	476.21 P>3.00	sts-N94741		ESTs
	476.64 P0.28	stSG22488		ESTs
	476.85 P0.36	stSG44909		ESTs
	477.06 P0.10	stSG54797		ESTs
	477.27 P1.33	stSG48099		ESTs
	477.37 P0.09 *	sts-AA028894		Homo sapiens silencing mediator of retinoic..
	477.80 P1.44	stSG52727		EST
	477.80 "	U44799		Human U1-snRNP binding protein homolog mR..
	477.80 "	WI-15963		ESTs
	477.80 "	stSG53886		ESTs, Weakly similar to neuronal thread pr..
	478.74 P0.01	WIAF-364		ESTs
	479.01 P0.21	WI-21080		ESTs
	479.13 P0.19	A009B29		ESTs
	479.33 P0.22	A006F32	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19	WIAF-449	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19 *	WI-15890		H.sapiens mRNA for transmembrane protein r..
	479.55 P0.20 *	stSG349		H.sapiens mRNA for transmembrane protein r..
	479.55 " *	A004O46	BDKRB2	bradykinin receptor B2
	479.55 "	stSG42540		ESTs
	479.55 "	sts-N26791		ESTs
	479.55 "	stSG53943		ESTs
	479.55 "	stSG49468		EST
145.7	479.74 P0.16	AFM294ze9	D12S342	Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694		EST
147.5 =	481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1

Next interval down

FIG. 2 I

Chromosome 12: D12S340-D12S97



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

Physical size of bin: 13 cR3000

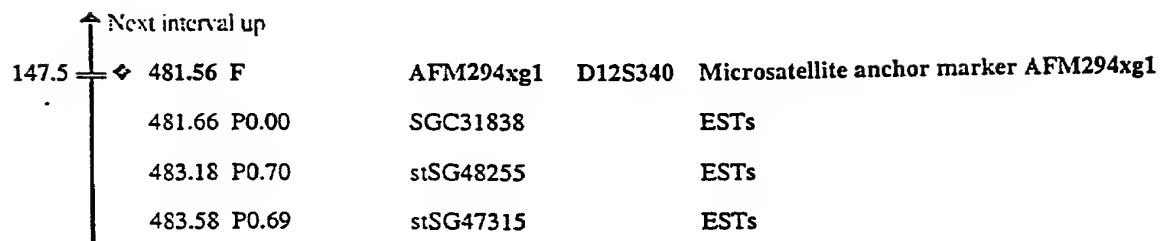


FIG. 2 J

483.87 P0.83	stSG47707	ESTs
484.70 P0.93	stSG4060	ESTs
484.70 "	stSG62390	GTF2H3 general transcription factor IIH, polypepti..
484.70 "	stSG42994	ESTs
484.73 P0.74	stSG46906	ESTs
484.80 P0.91	A004X33	ESTs
484.91 P1.11	stSG3211	ESTs, Weakly similar to B-cell growth fact..
484.91 " *	sts-Z41302	BDKRB2 bradykinin receptor B2
484.91 " *	sts-Z41302	BDKRB2 bradykinin receptor B2
484.91 "	sts-T58259	ESTs, Weakly similar to B-cell growth fact..
484.91 "	stSG52737	ESTs
484.91 "	Bda03b10	UBC ubiquitin C
484.91 "	stSG1936	CD36L1 CD36 antigen (collagen type I receptor, thr..
484.91 "	sts-AA017225	ESTs
484.91 P1.15	WI-12212	ESTs
485.12 P1.18	A004F14	ESTs
485.12 P1.18	SGC31333	ESTs
485.23 P1.21 *	WI-12482	BDKRB2 bradykinin receptor B2
485.23 P1.07	sts-AA017698	ESTs
485.33 P1.22	WI-12422	ESTs
485.51 P1.18	stSG42398	EST
485.64 P1.04	sts-AA009669	ESTs
486.07 P2.50	stSG21539	EST
486.13 P1.44	WI-12439	EST
486.34 P1.26	sts-W31616	UBC ubiquitin C
486.38 P>3.00	stSG54715	ESTs
486.76 P1.64 *	WI-6921	H.sapiens mRNA for transmembrane protein r..
487.08 P>3.00	WI-13120	Human mRNA for KIAA0318 gene, partial cds
487.23 P>3.00	stSG54353	ESTs
487.23 P>3.00	stSG22703	EST
487.28 P>3.00	stSG62698	ESTs
487.28 P>3.00 *	sts-D60472	Homo sapiens silencing mediator of retinoic..
487.28 P>3.00	stSG36097	ESTs
487.33 P1.36	sts-U37146	Homo sapiens silencing mediator of retinoic..

FIG. 2 K

154.4	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
160.9	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
	◆ 489.07 P>3.00	AFMa123xe1	D12S367 Microsatellite marker AFMa123xe1
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37	*** Cdalad08	ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

FIG. 2 L

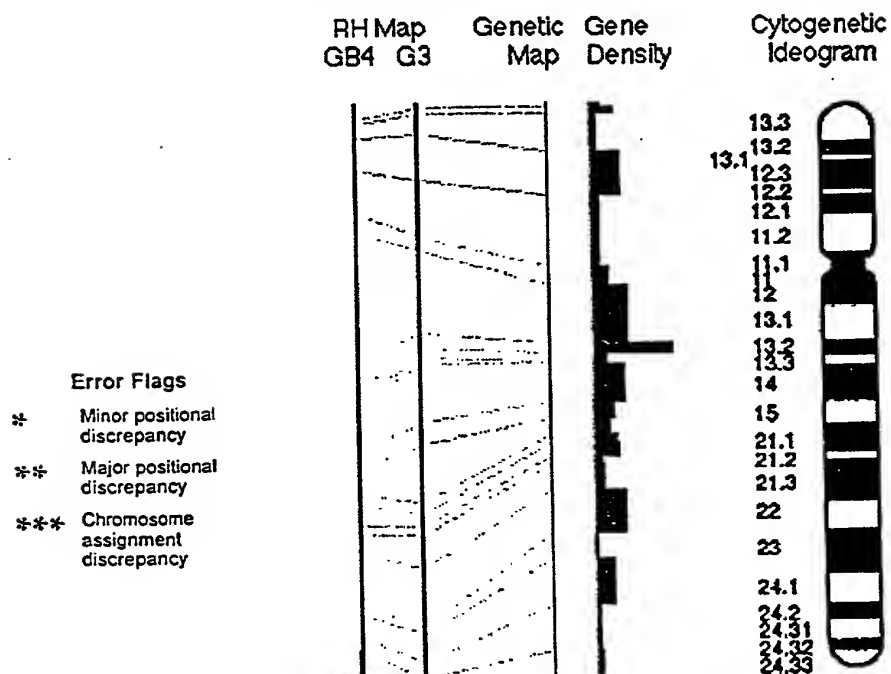
160.9 —◆ 494.19 F
 ↓ Next interval down

stSG43910	SFRS8	splicing factor, arginine/serine-rich 8 (sup..
AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6

160.9 —◆ 494.19 F
 ↓ Next interval down

FIG. 2 M

Chromosome 12: D12S97-qTEL



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: 172 cR3000

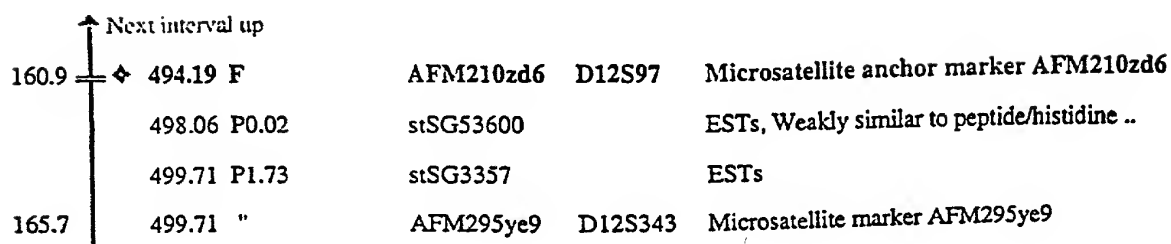


FIG. 2 N

499.71 P1.72	stSG30906	ESTs	
499.71 "	stSG43796	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769	ESTs	
500.50 P1.88	stSG26056	ESTs	
500.50 P2.33	SGC30786	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG1702		Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820	ESTs	
500.61 "	stSG42115	KIAA0331	KIAA0331 gene product
500.61 "	IB2452	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521	ESTs	
500.61 "	FB9F8		ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357	ESTs	
500.61 "	stSG4720		Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG31443	ESTs	
500.61 P>3.00	stSG49622	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559	ESTs	
501.04 P1.10	stSG54842	ESTs	
501.04 P2.03	A008Y05	Unknown	
501.89 P2.18	stSG39493		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865	EST	
501.99 P>3.00	R50113	ESTs	
502.10 P1.75	stSG48386	ESTs	
502.10 "	stSG50504	ESTs	
502.63 P0.06	A006R19	ESTs	
502.63 P1.06	WIAF-864	ESTs	
502.94 P1.51	stSG54813		ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47		ESTs, Highly similar to DNA polymerase ep..
503.25 P0.28	stSG27206	ESTs	
503.25 "	stSG40199		Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935	ESTs	
504.68 P0.69	stSG4731		Homo sapiens mRNA for KIAA0692 protein, p..

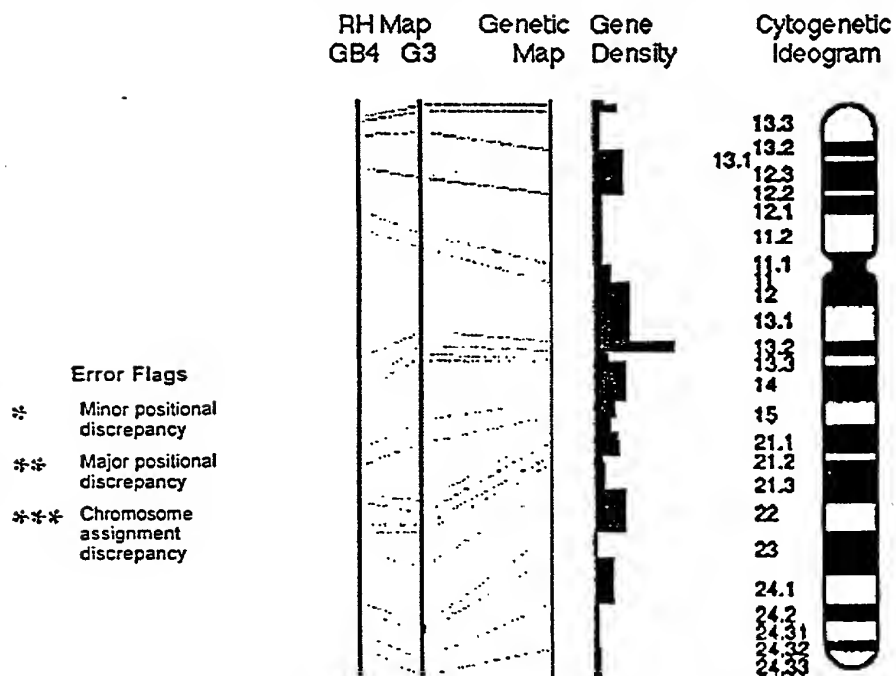
FIG. 2 O

169.1

504.68 "	A005Q05		ESTs
504.68 "	stSG8142		ESTs, Highly similar to DNA polymerase ep..
506.39 F	AFM310vd5	D12S357	Microsatellite marker AFM310vd5
506.39 P0.02	A005X42		Homo sapiens mRNA for KIAA0692 protein, p..
508.59 P0.78	Cda18g06		ESTs
◆ 508.59 P0.78 **	Cda1jf08		Homo sapiens mRNA for GCP170, complete cd..
508.59 P0.54	R39599		ESTs
509.98 P0.10	stSG31494	ZNF140	zinc finger protein 140 (clone pHZ-39)
509.98 P0.16	stSG40222		ESTs
509.98 "	sts-R55615		ESTs, Weakly similar to zinc finger protei..
509.98 "	sts-R02295		ESTs
509.98 "	sts-R81342		ESTs
511.20 F	TEL-12q82		Marker TEL-12q82
512.81 P0.20	sts-H65839		ESTs, Weakly similar to transformation-rel..
514.97 P0.36	stSG46141		ESTs, Weakly similar to zinc finger protei..
514.97 P0.90	stSG52998		ESTs
519.10 P1.77	A008W21	CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
519.54 P0.81	stSG52716		ESTs
● TELOMERE			

FIG. 2 P

Chromosome 12: D12S79-D12S366



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S79 (126.1 cM)
 Bottom of interval: D12S366 (133.8 cM)
 Genetic size of bin: 8 cM
 Physical size of bin: 63 cR10000

FIG. 3 A

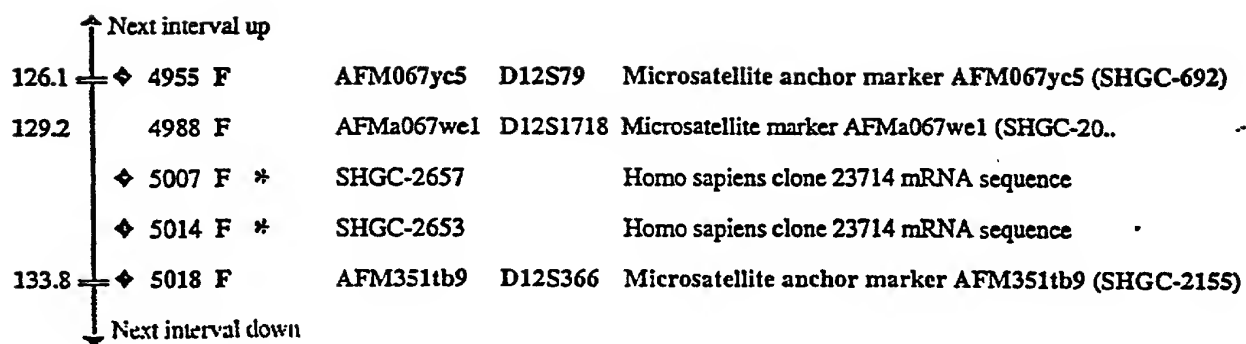
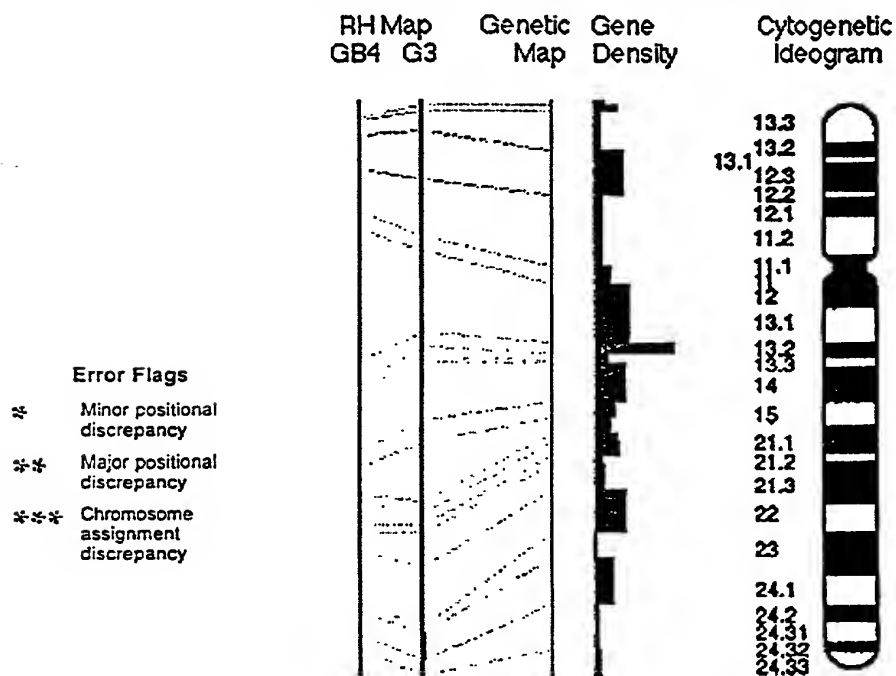


FIG. 3 B

Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

Physical size of bin: 261 cR10000

FIG. 3 C

				Next interval up
133.8	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1	5047 F	AFMa225xe5	D12S1619	Microsatellite marker AFMa225xe5 (SHGC-20..
	◆ 5085 F	SHGC-33949	KIAA0262	KIAA0262 gene product
	◆ 5089 F	SHGC-10488	KIAA0152	KIAA0152 gene product
	◆ 5093 F	SHGC-10346		Homo sapiens HSPC004 mRNA, complete cds
	◆ 5098 F	SHGC-13898		Homo sapiens HSPC004 mRNA, complete cds
137.5	◆ 5163 F	AFM220zf4	D12S321	Microsatellite marker AFM220zf4 (SHGC-212..
	5199 F	SHGC-11702		ESTs
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)
				Next interval down

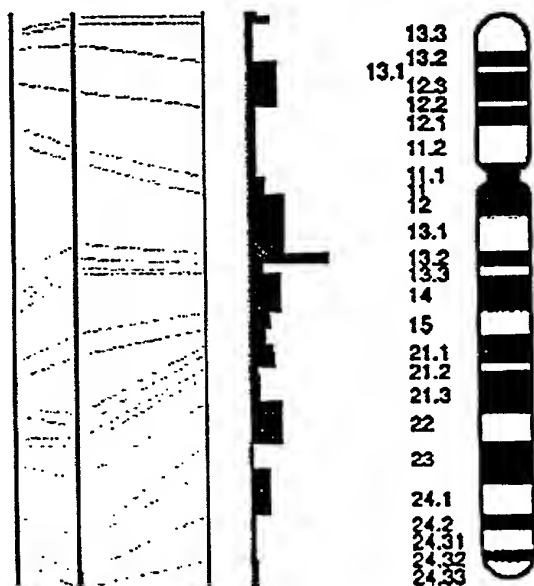
FIG. 3 D

Chromosome 12: D12S340-D12S97

RH Map Genetic Gene Cytogenetic
GB4 G3 Map Density Ideogram

Error Flags

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

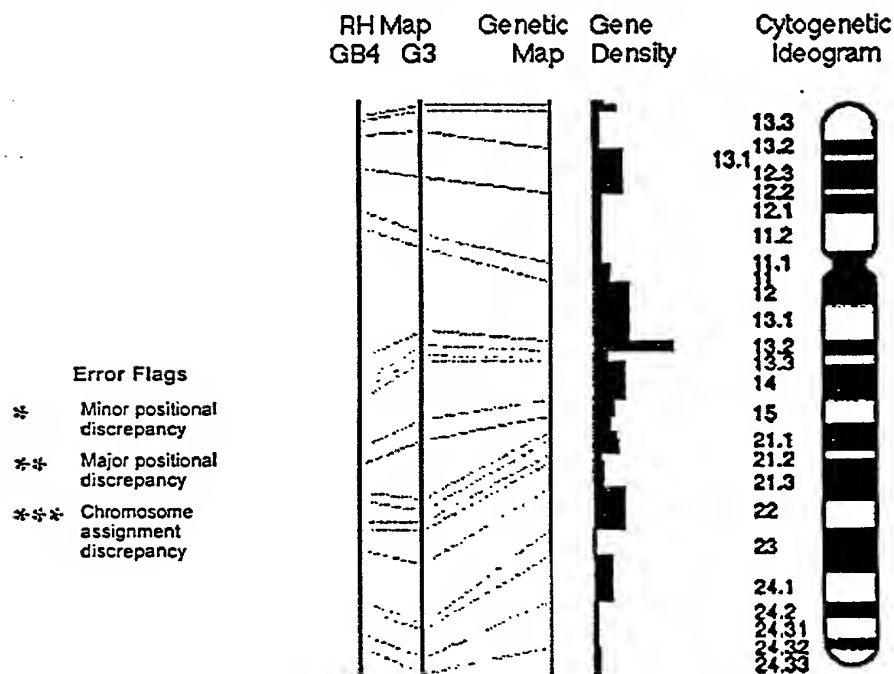
Physical size of bin: 151 cR10000

FIG. 3 E

Position (cM)	Marker	Marker Name	Marker Type	Marker Description
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..)
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..)
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..)
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..)
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..)
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)

FIG. 3 F

Chromosome 12: D12S97-qTEL



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: -4429 cR10000

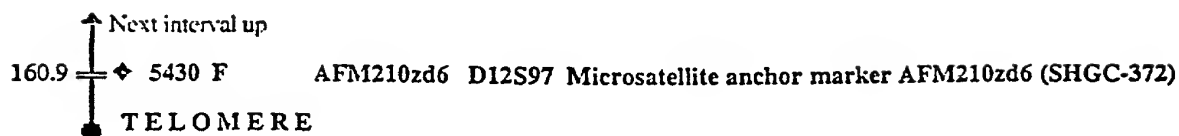


FIG. 3 G

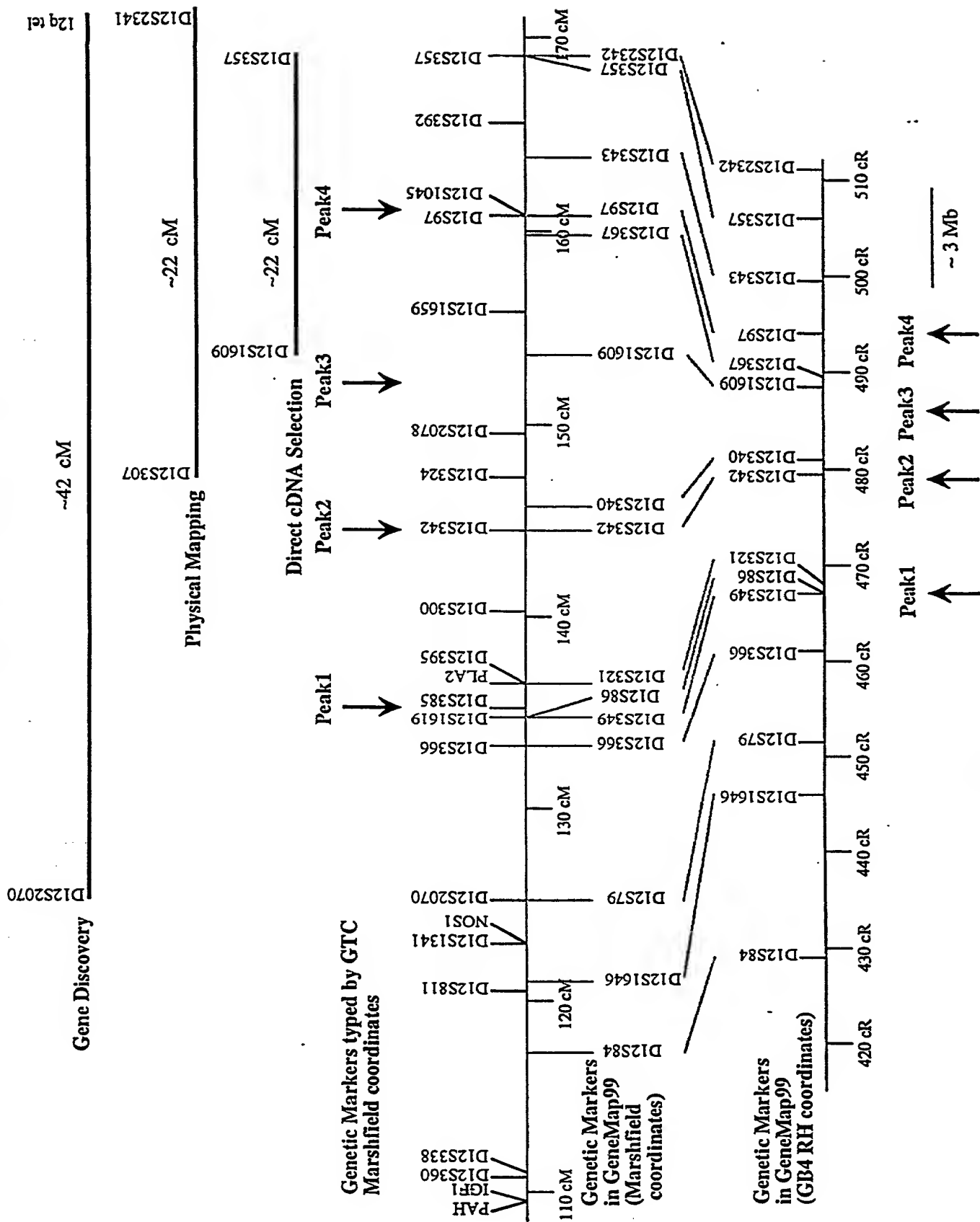


FIG. 4

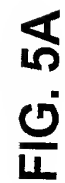


FIG. 5A

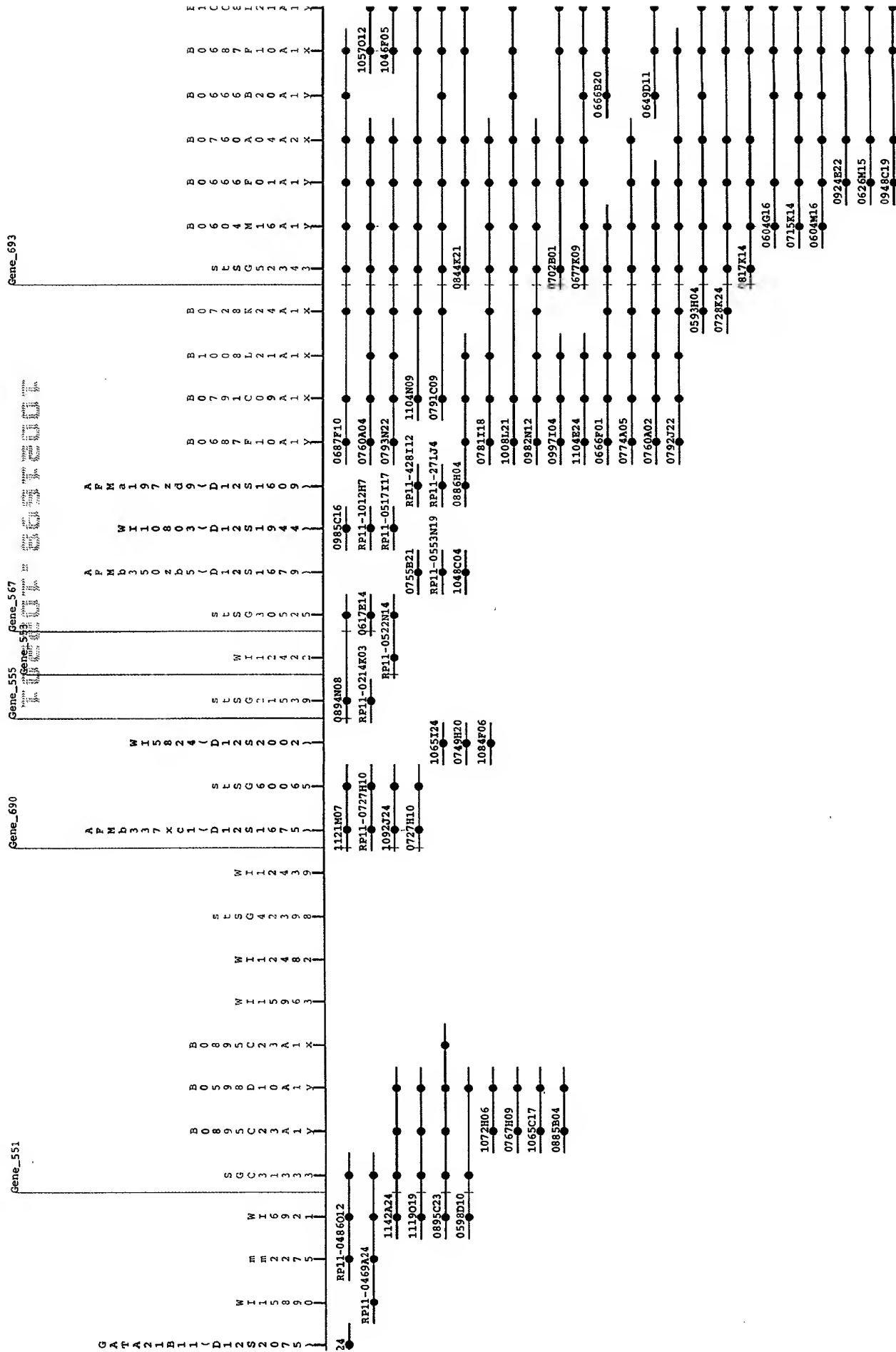


FIG. 5B

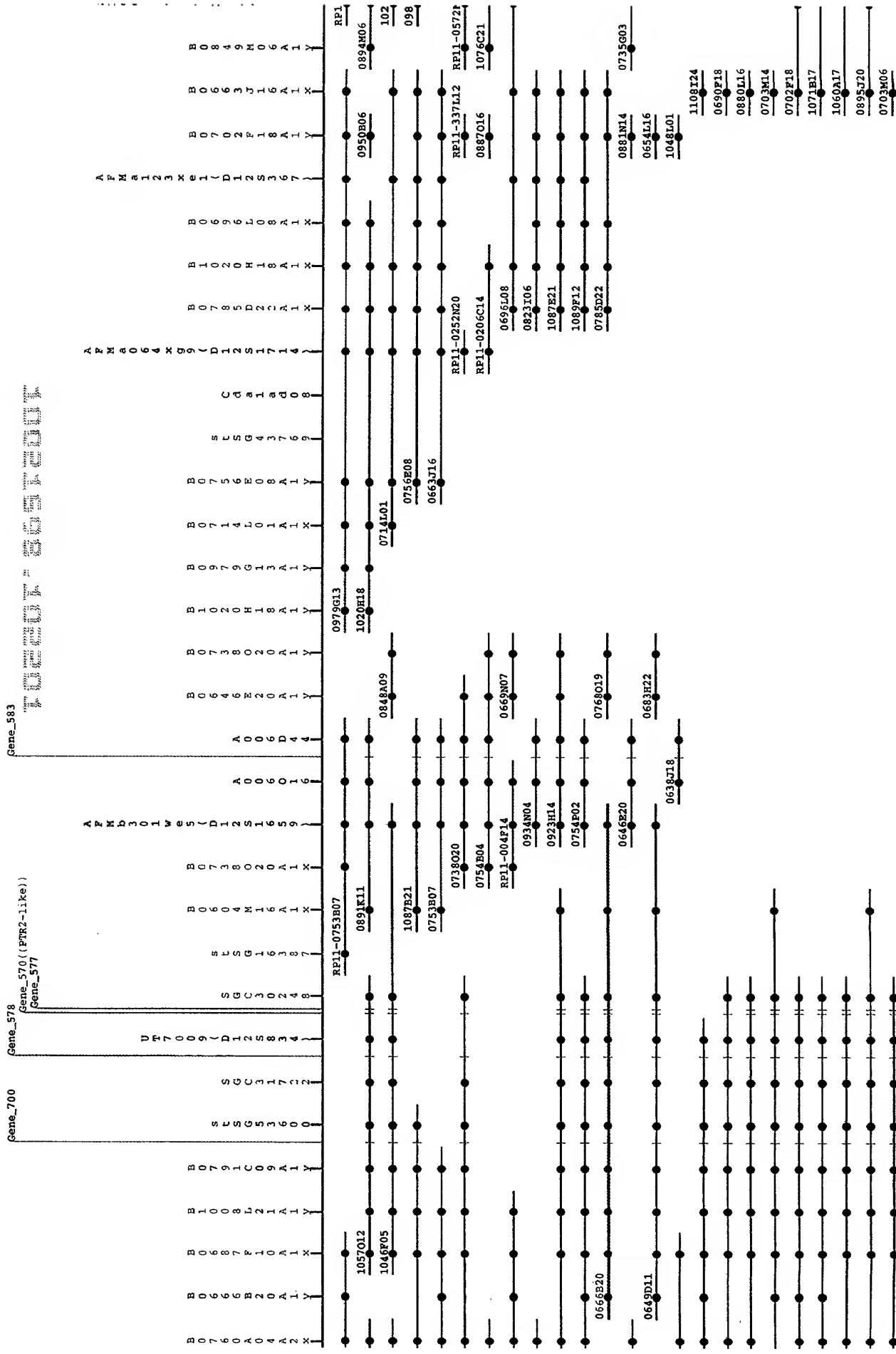


FIG. 5C

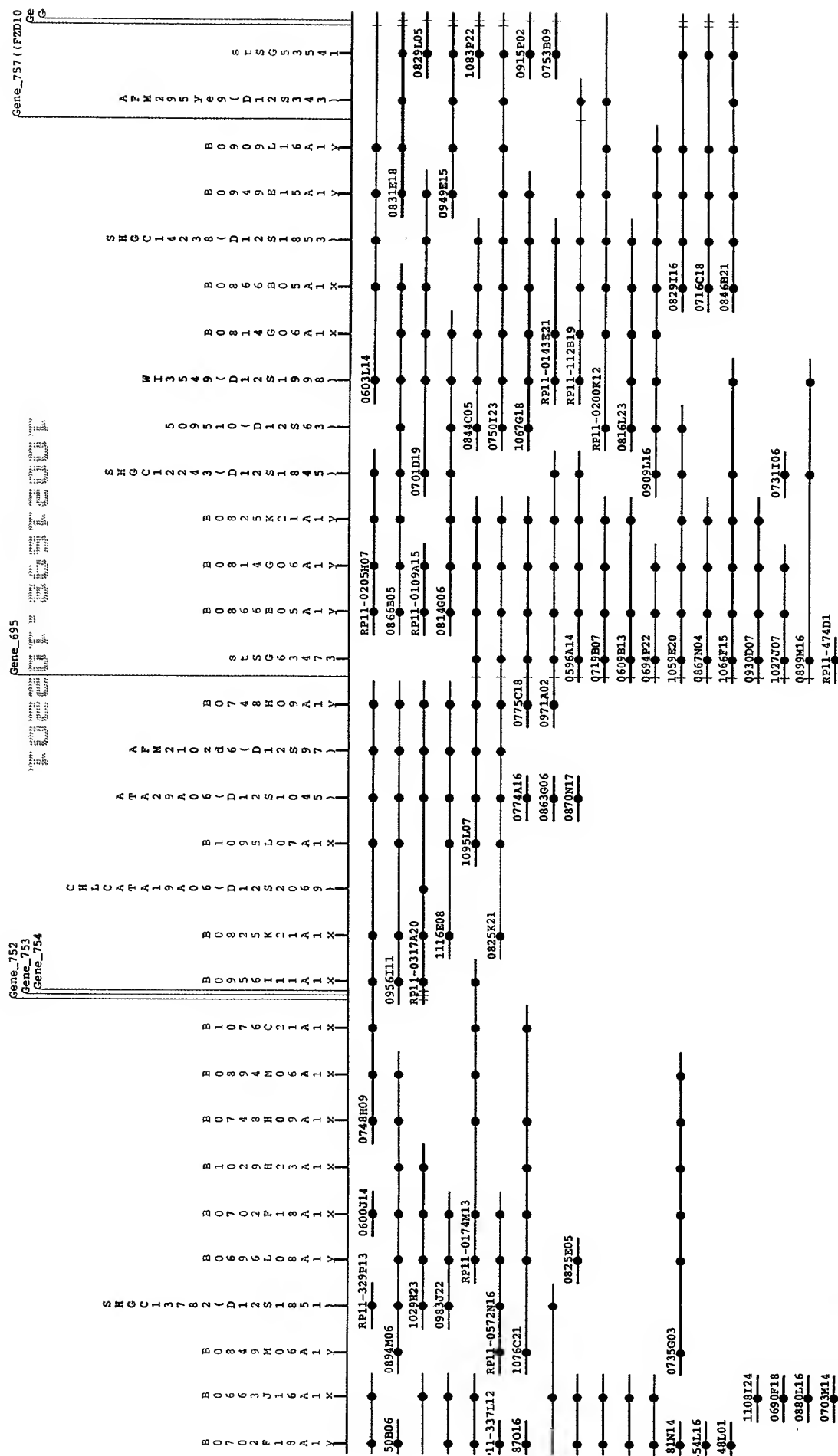
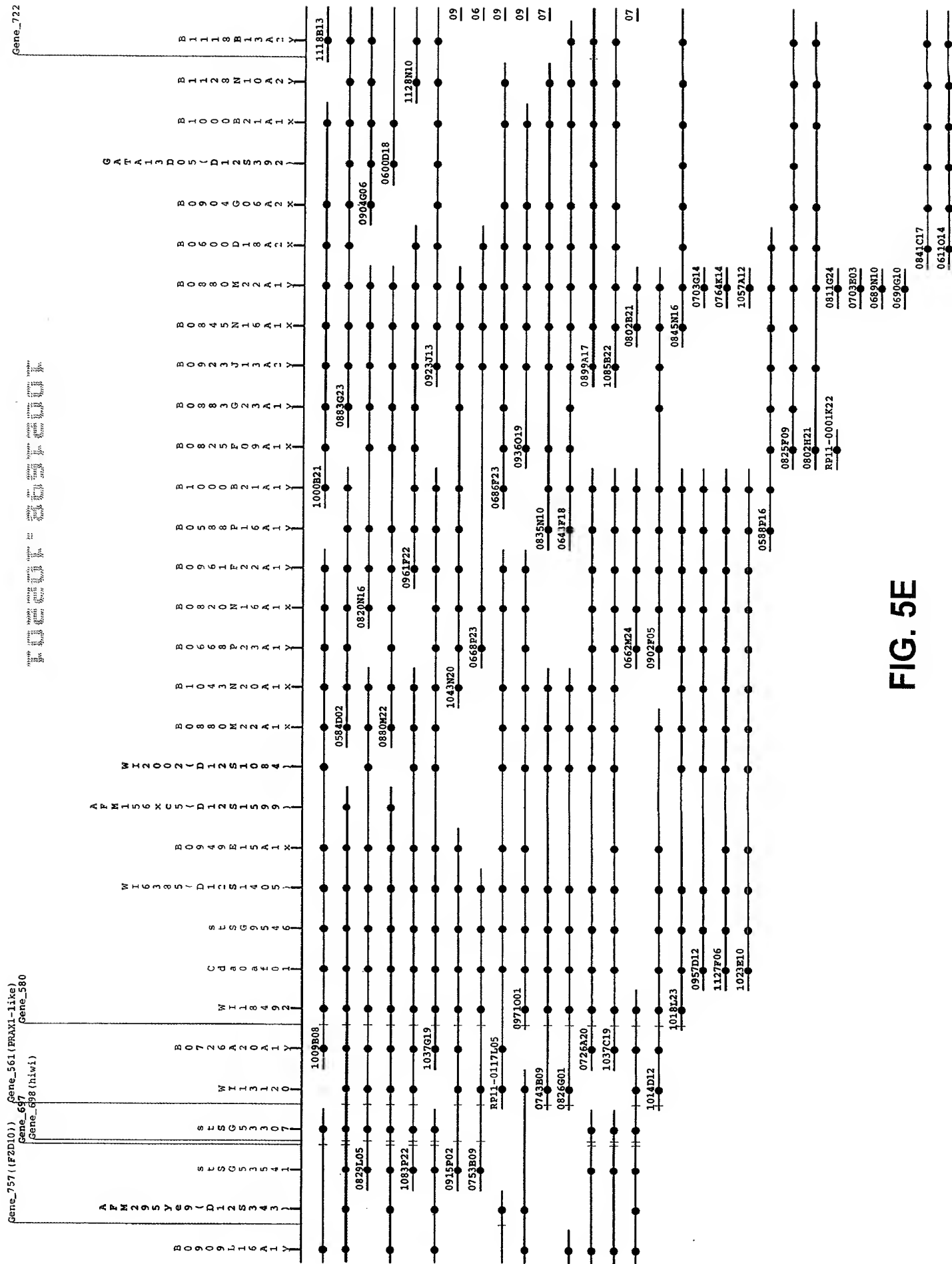


FIG. 5D



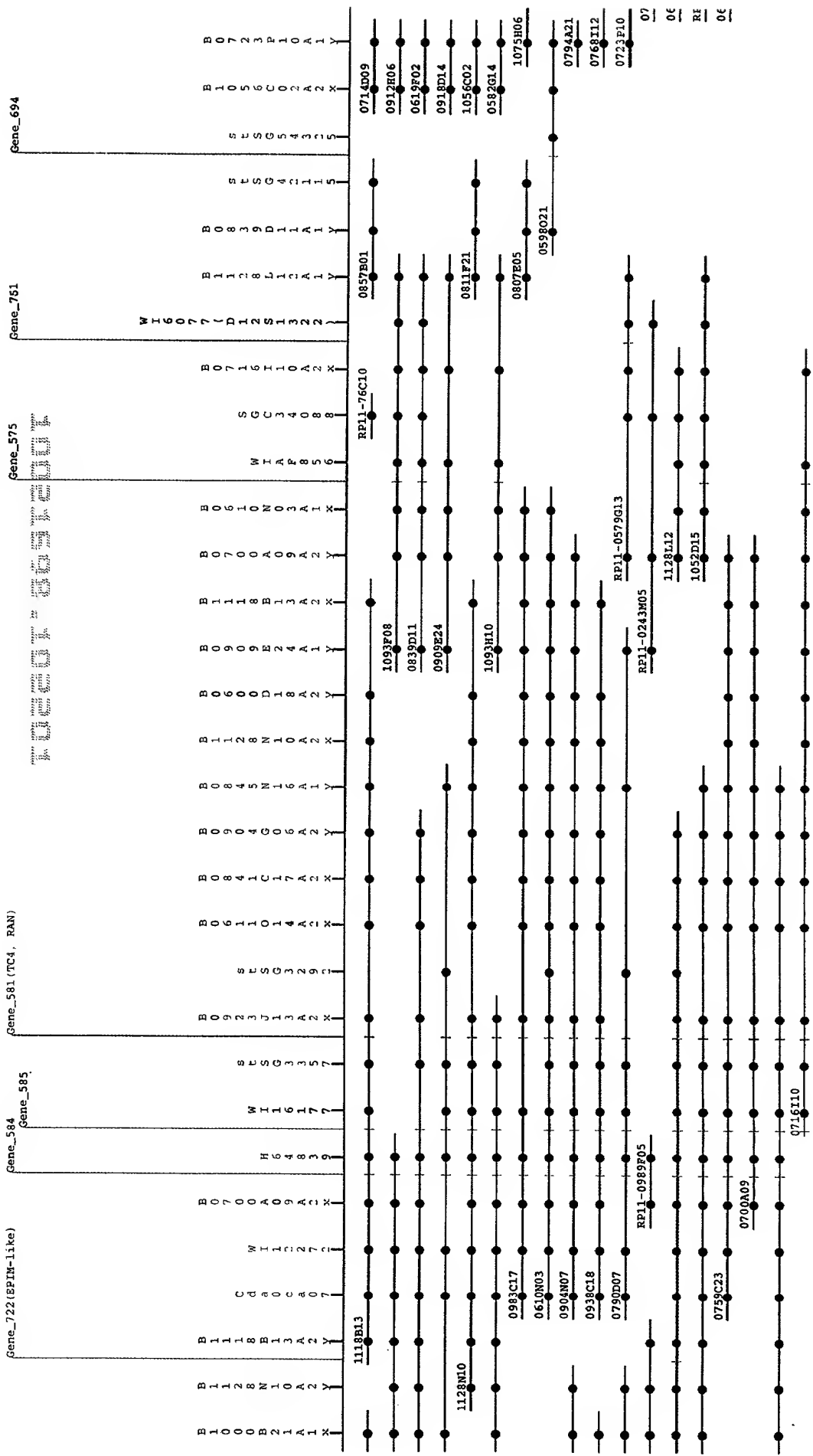
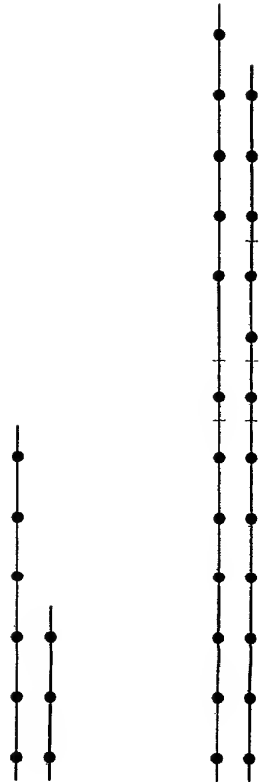


FIG. 5F



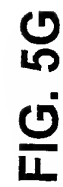


FIG. 5G

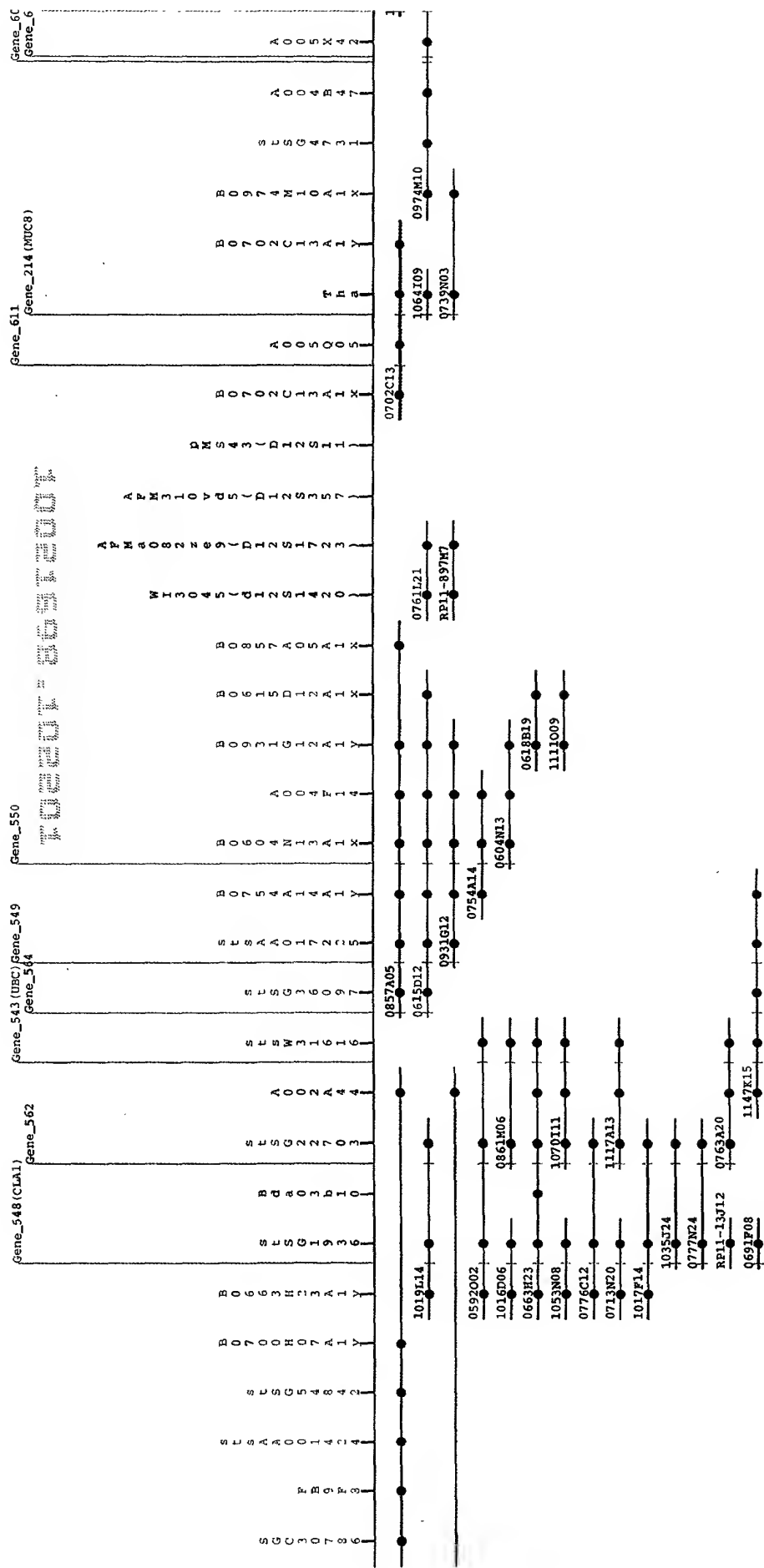


FIG. 5H

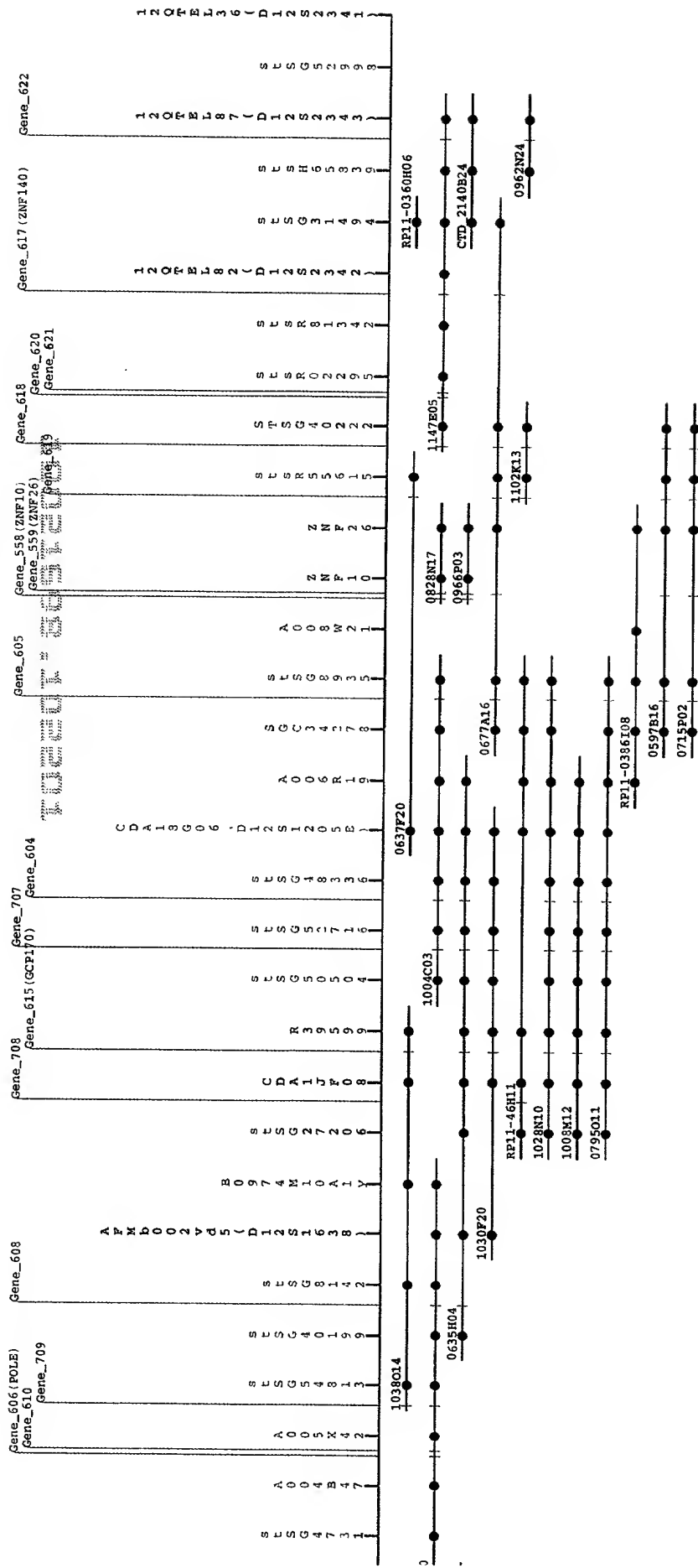
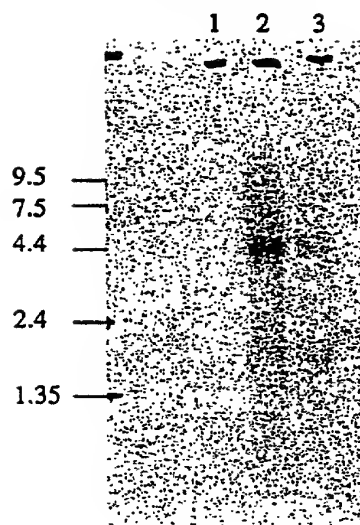


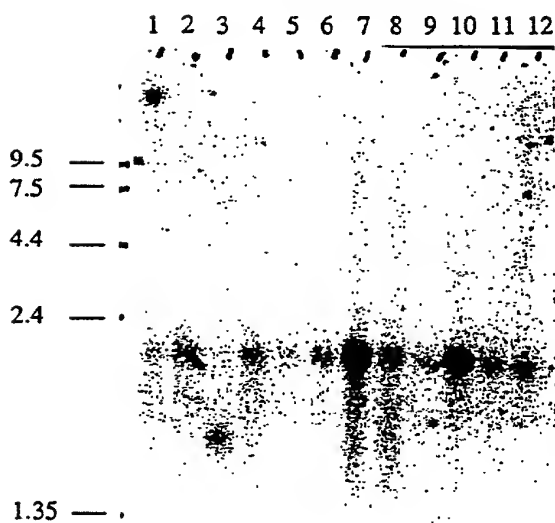
FIG. 5I

Gene 214



1. Lymphoblastoid cell line
2. Lung
3. Trachea

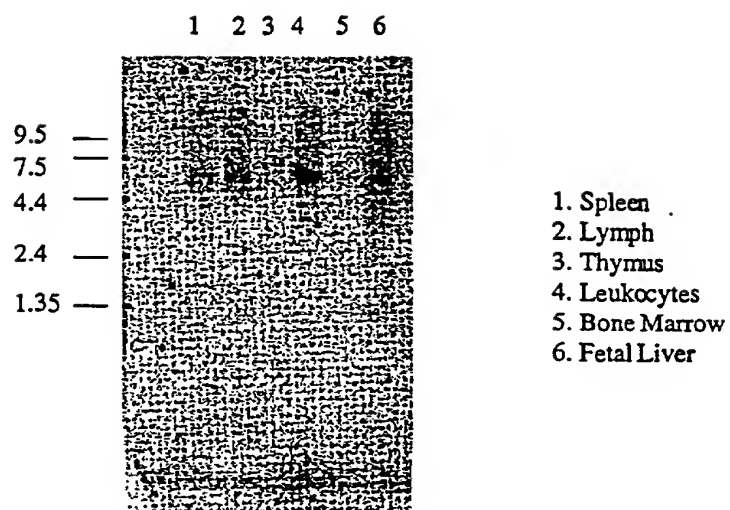
Gene 436



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 A

Gene 454



Gene 515

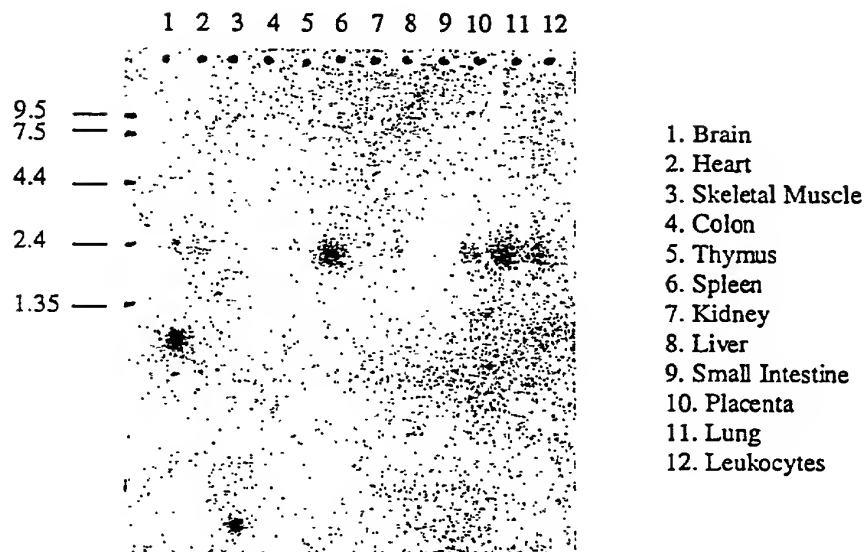
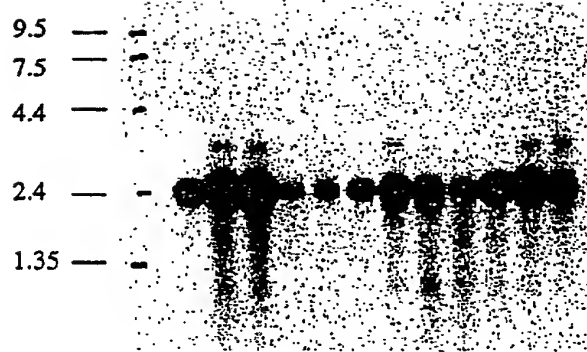


FIG. 6 B

Gene 543

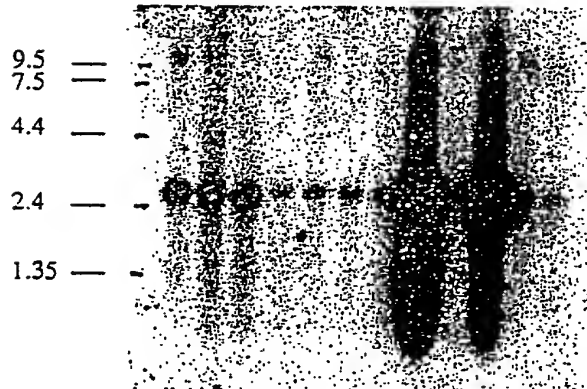
1 2 3 4 5 6



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

Gene 548

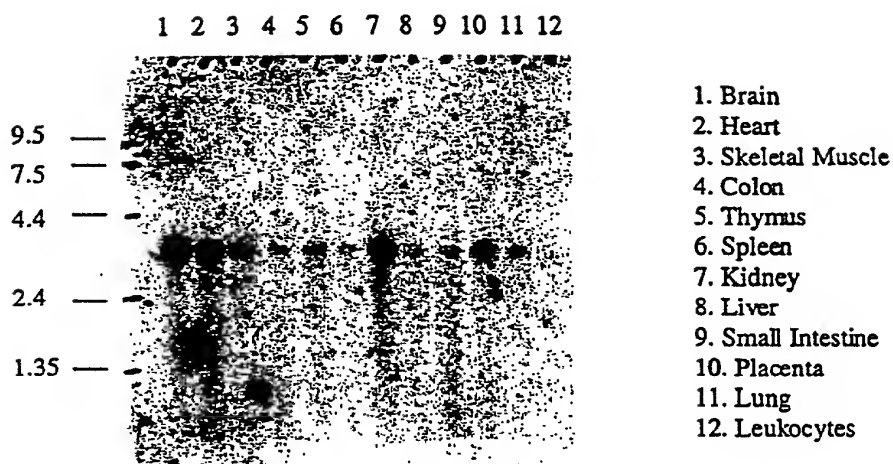
1 2 3 4 5 6 7 8 9 10 11 12



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 C

Gene 550



Gene 561

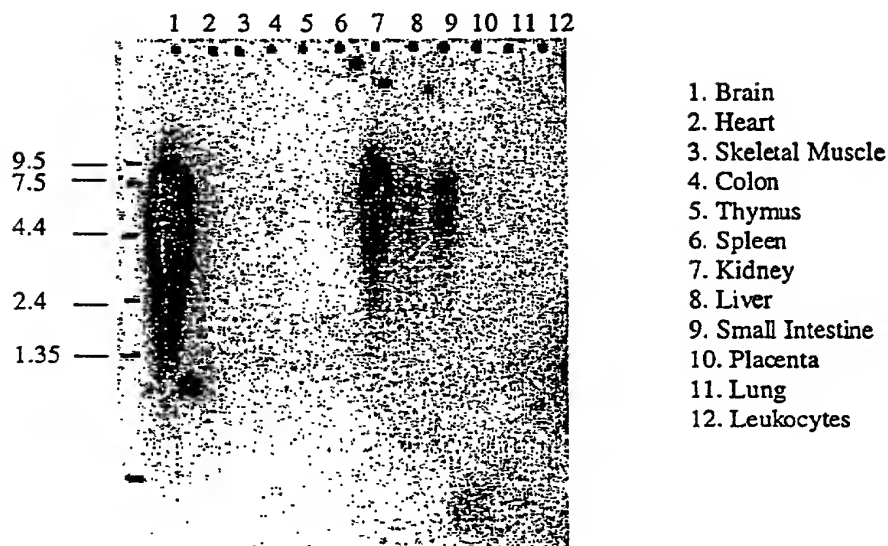
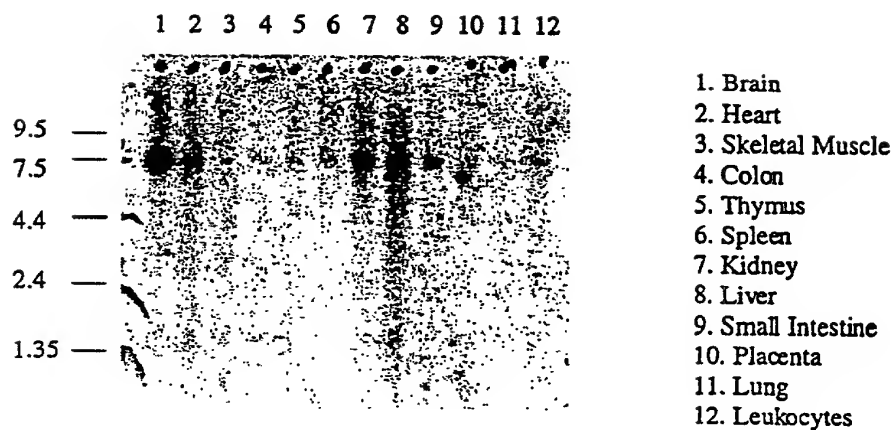


FIG. 6 D

Gene 564



Gene 570

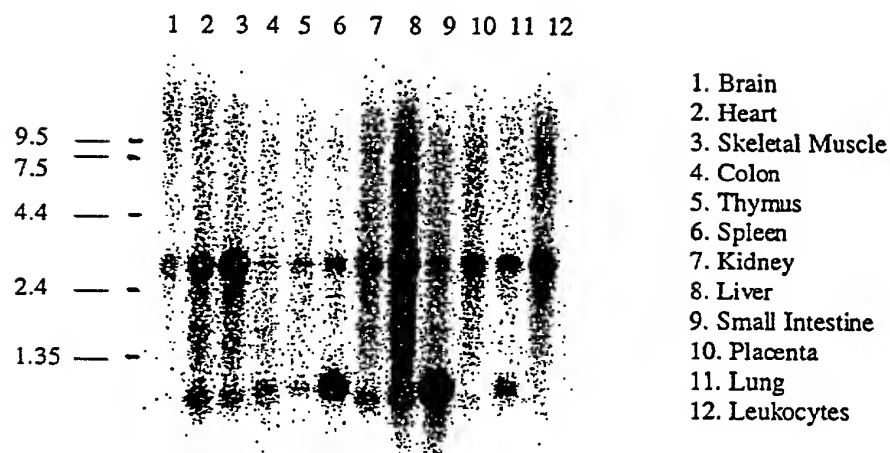
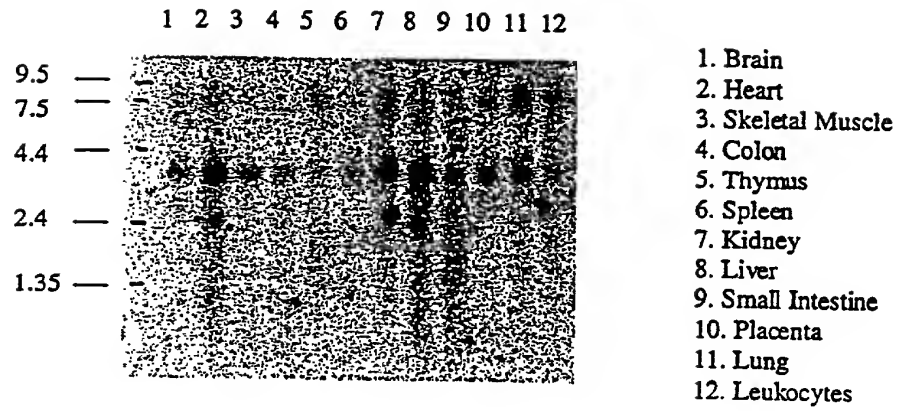


FIG. 6 E

Gene 576



Gene 577

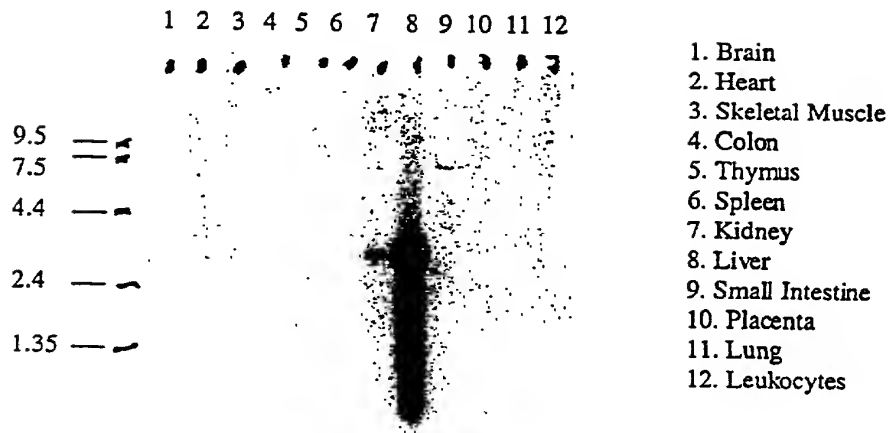
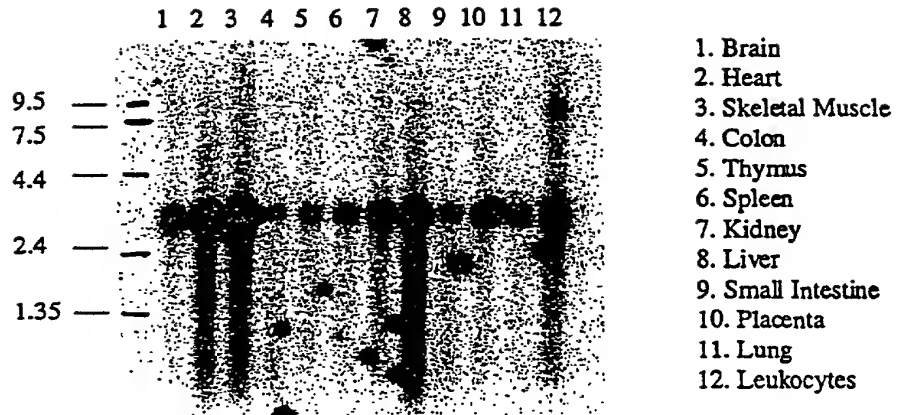


FIG. 6 F

Gene 578



Gene 579

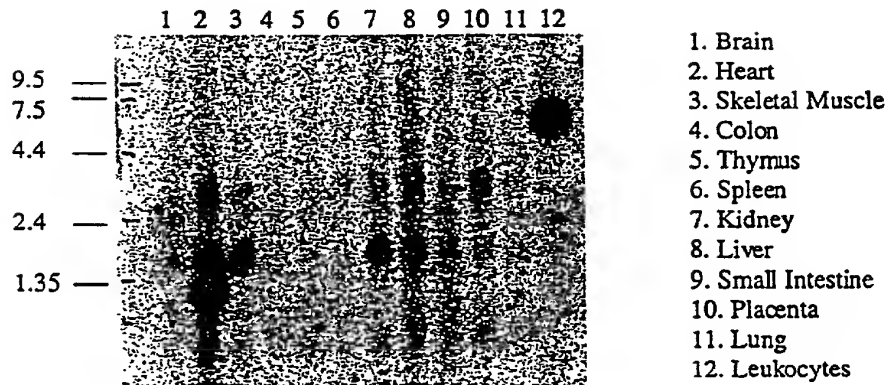
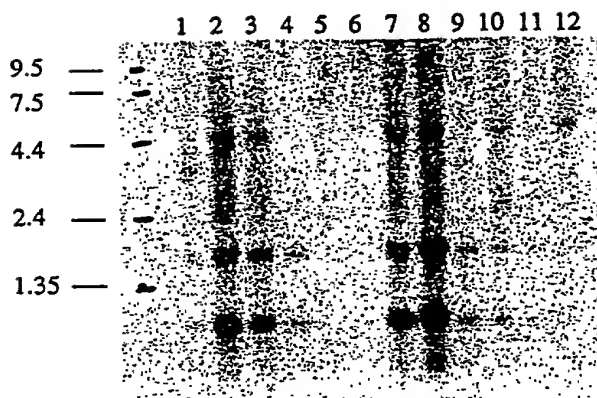


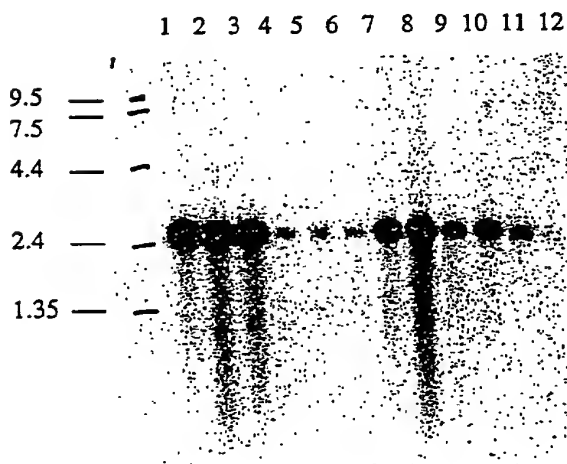
FIG. 6 G

Gene 580



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

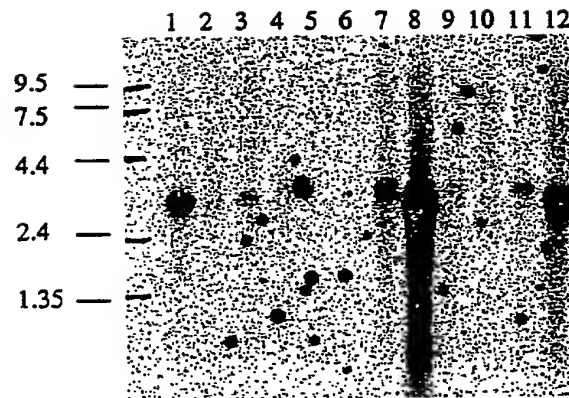
Gene 581



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

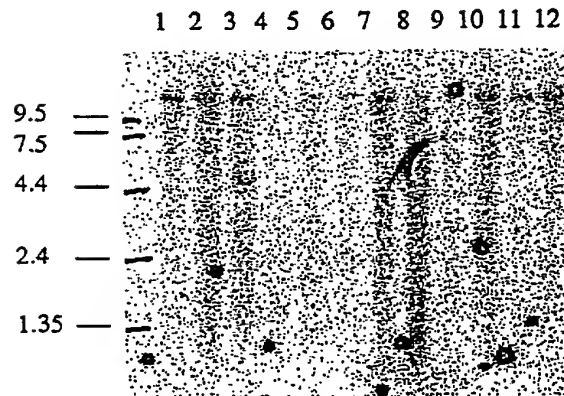
FIG. 6 H

Gene 583



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

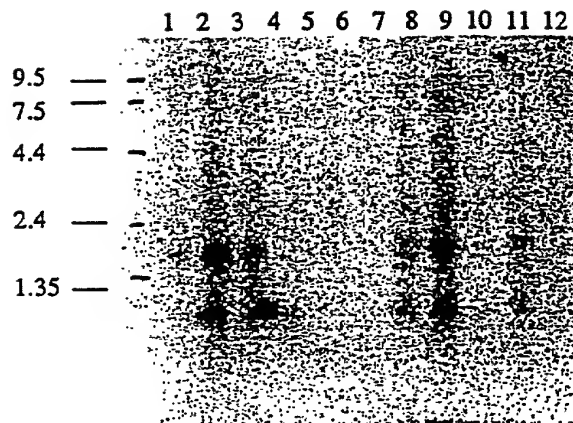
Gene 589



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

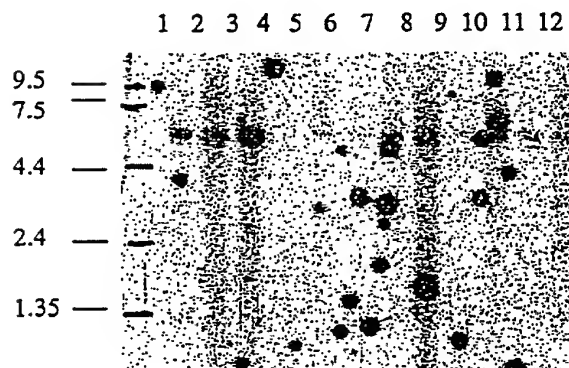
FIG. 6 I

Gene 590



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

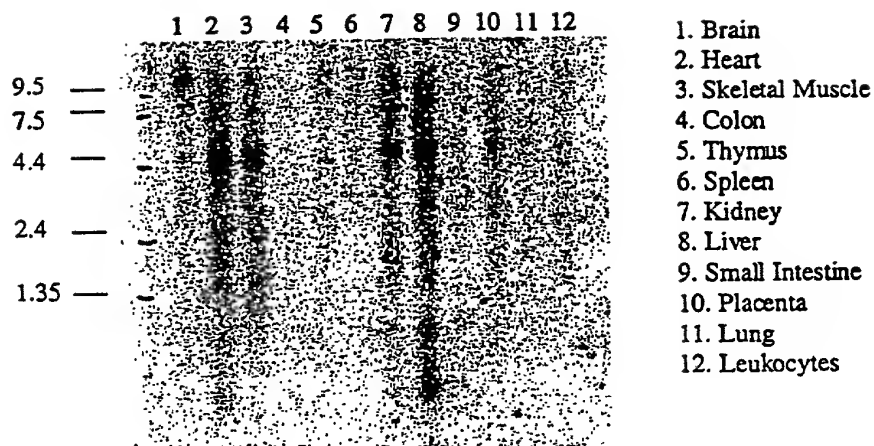
Gene 592



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 J

Gene 594



Gene 595

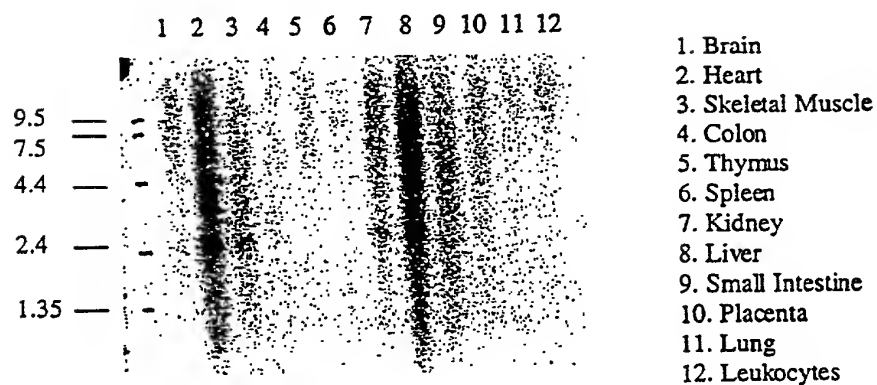
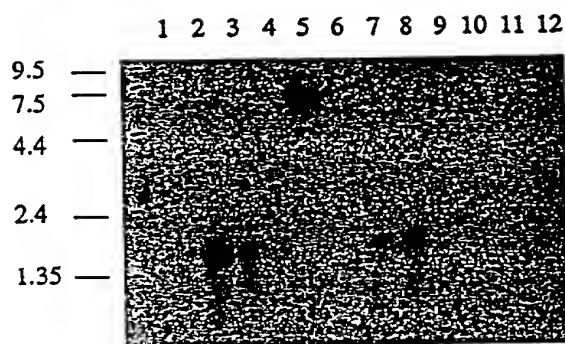


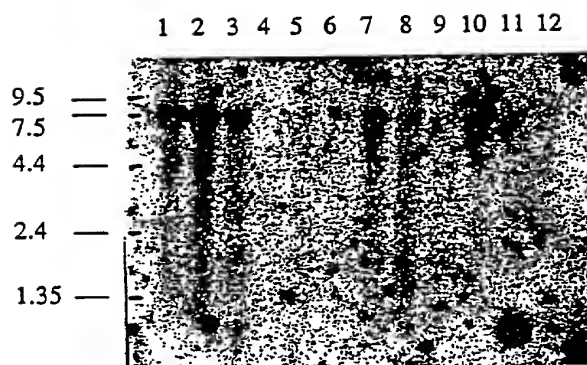
FIG. 6 K

Gene 596



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

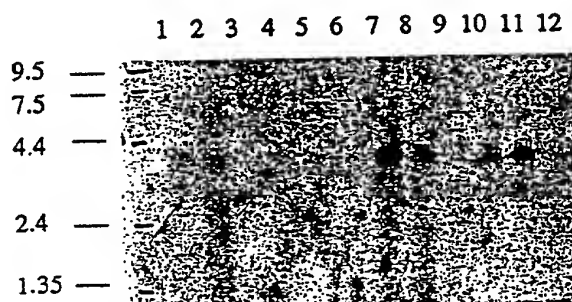
Gene 604



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

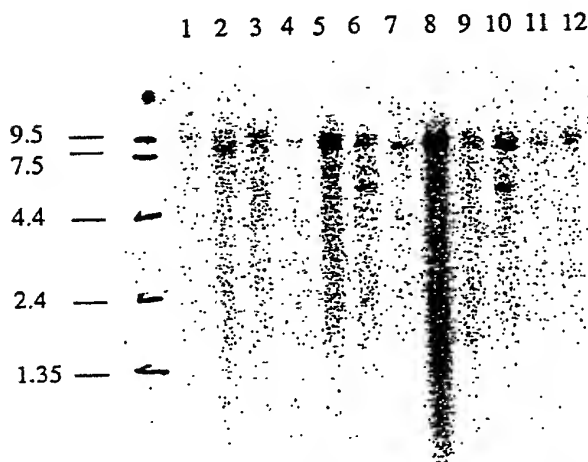
FIG. 6 L

Gene 605



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

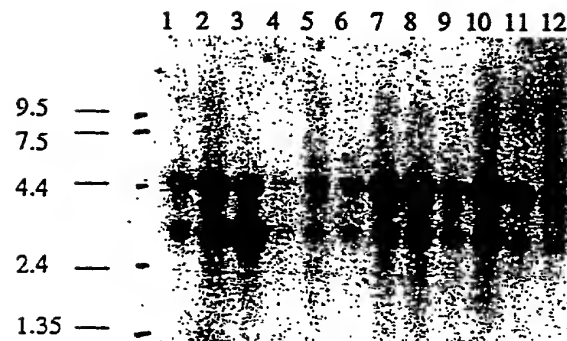
Gene 606



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

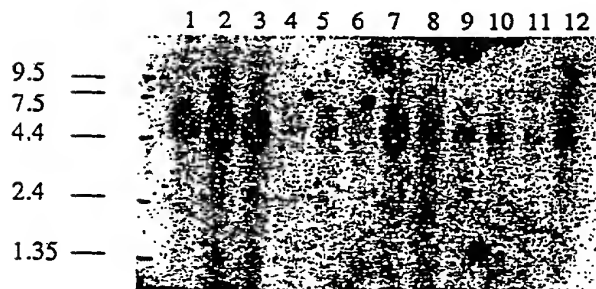
FIG. 6 M

Gene 608



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

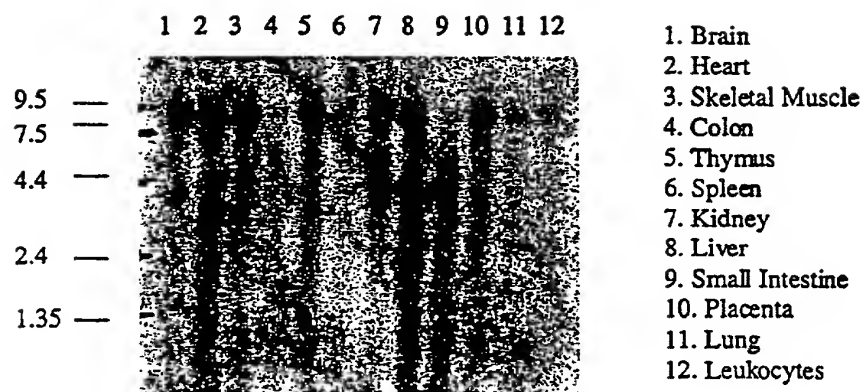
Gene 611



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 N

Gene 615



Gene 617

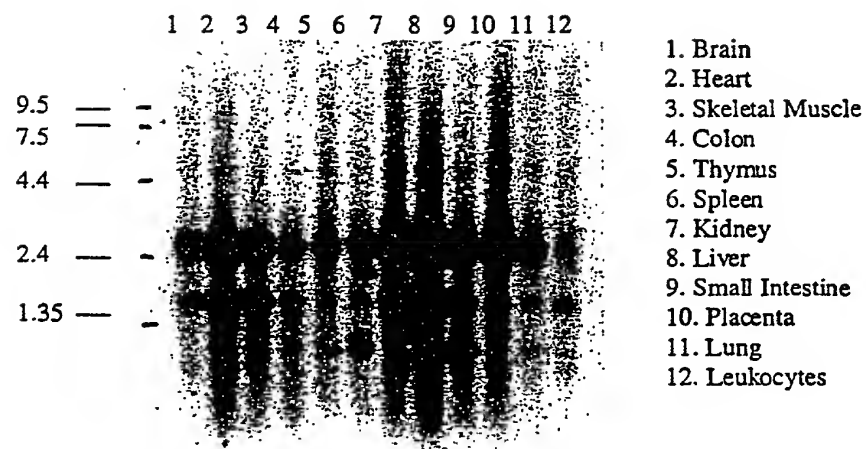
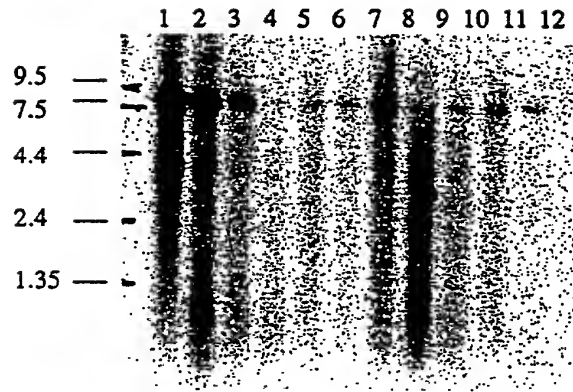


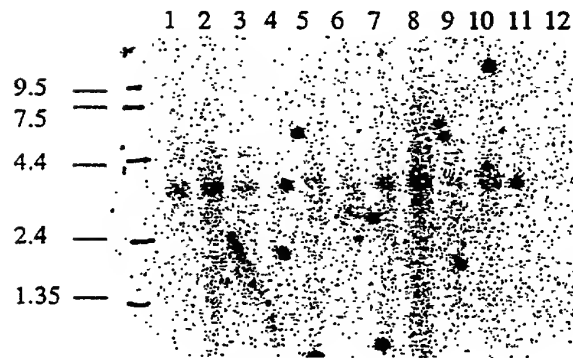
FIG. 6 O

Gene 618



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

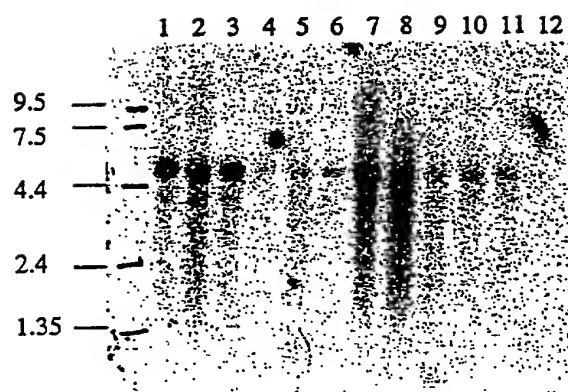
Gene 619



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

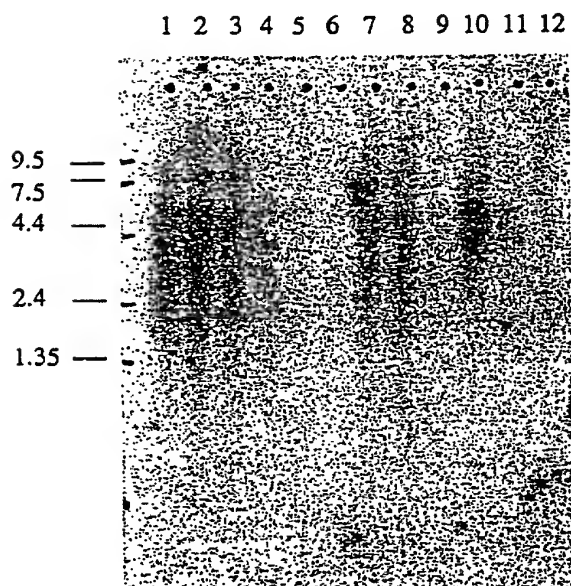
FIG. 6 P

Gene 621



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

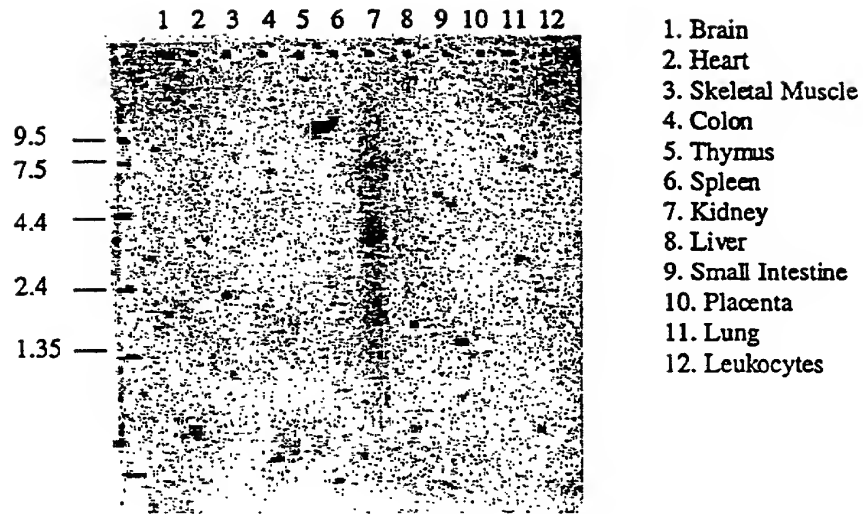
Gene 693



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 Q

Gene 698



Gene 699

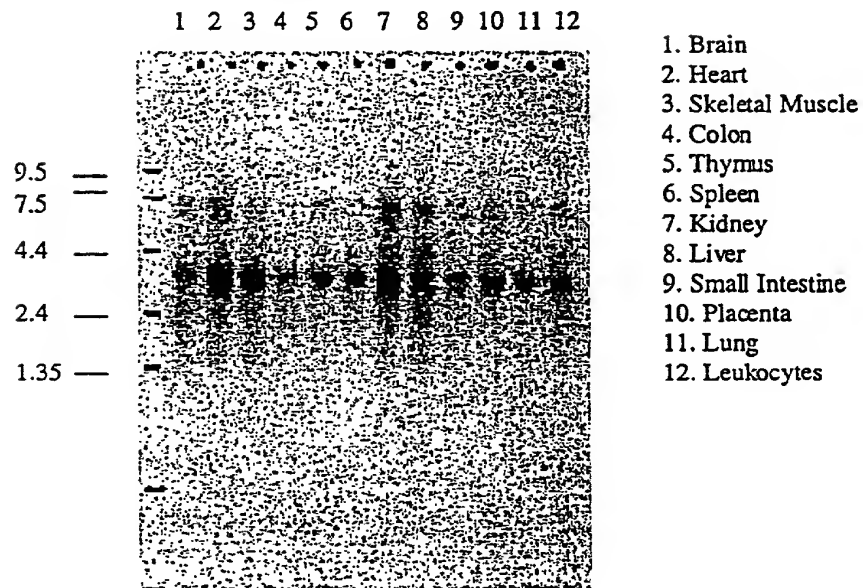
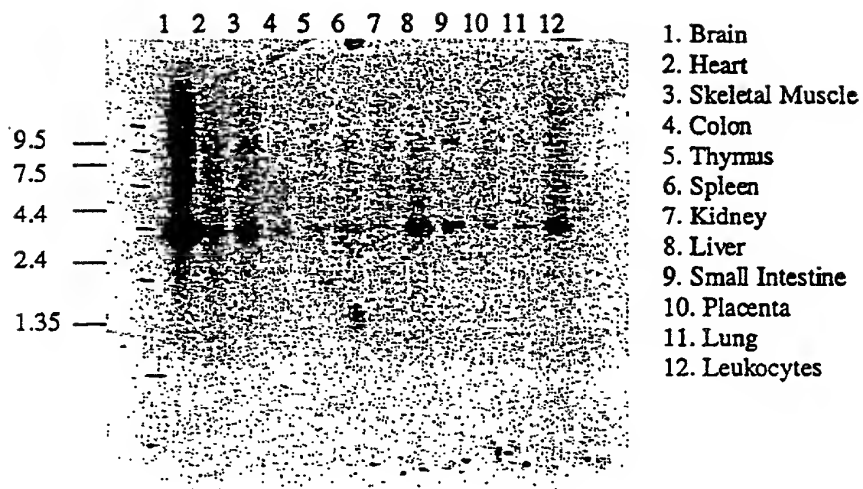


FIG. 6 R

Gene 702



Gene 722

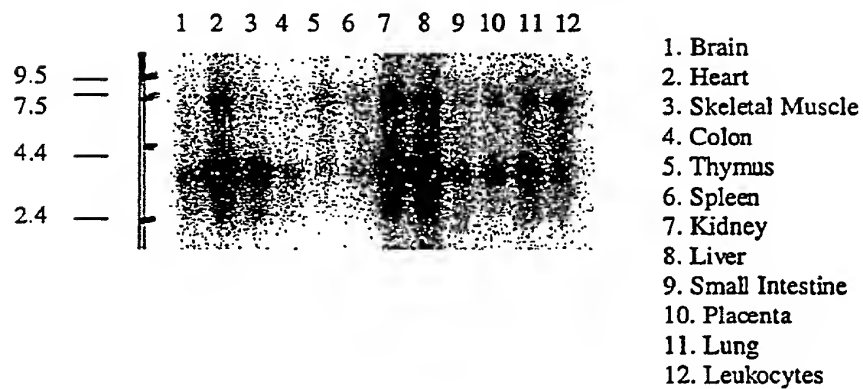
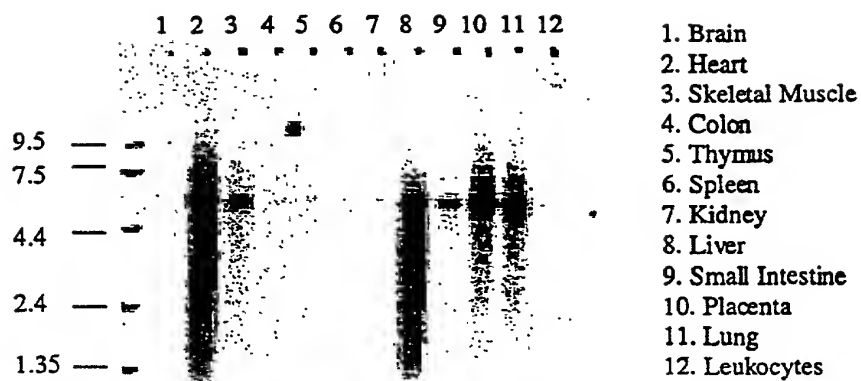


FIG. 6 S

Gene 751



Gene 756

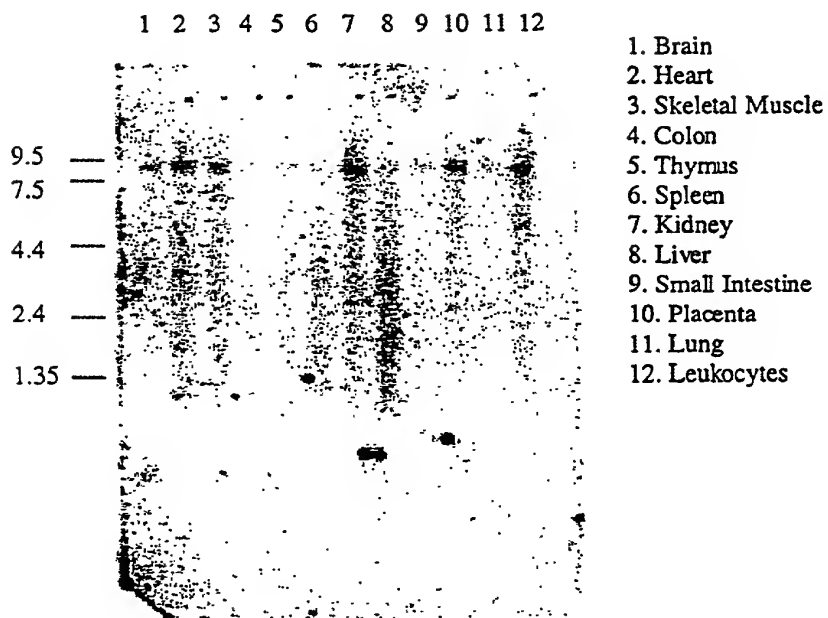
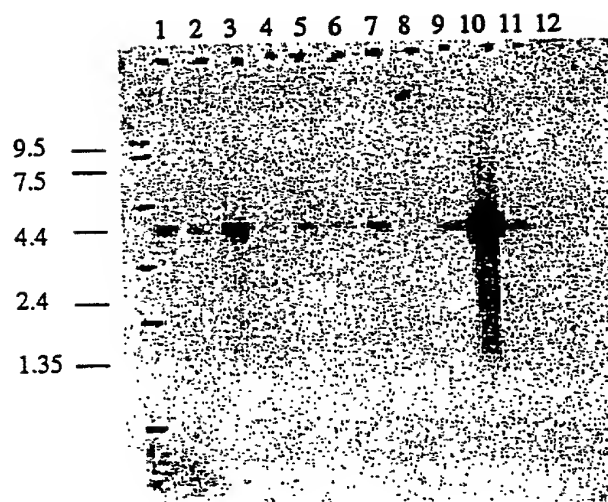


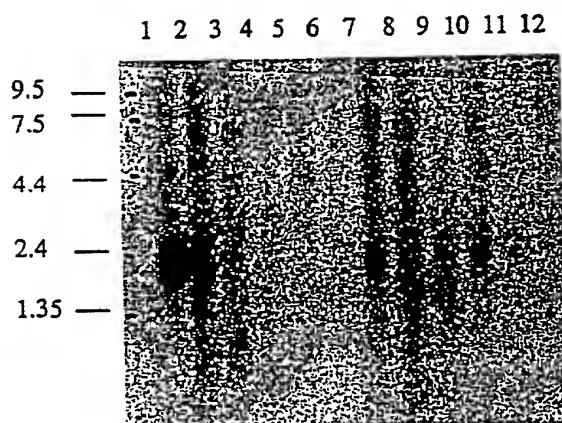
FIG. 6 T

Gene 757



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

Gene 848



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 U

AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCC
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

610 630 650
CGGCCTGCTCTCTTGAACAGTGCCGAAAACCTCACTGTGCTCATCAAGAACAATATCGAC
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670 690 710
TTCCCCGGCCACAACCTACACCACGAGAAACATCCTGCCAGGTTTAAACATCACTTGTACC
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730 750 770
TTCCACAAGACTCAGAATCCACAGTGTCCTTTCCGACTAGGAGACATCTTCCGAGAA
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790 810 830
ACAGGCGATAATTTTTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850 870 890
TGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCGTCCCAAATACAGTTTCCGTGCG
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910 930 950
CTTGACGACAAGACCACCAACGTGTCCTTGTTACCCTGGCTACAACCTCAGATACGCCAAG
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970 990 1010
TACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTT
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030 1050 1070
GACATCCTGGTTTTTGGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATC
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

1090 1110 1130
GGCTCAACCCTCTCCTACTTCGGTCTGGCCACTGTGTTCACTCGACTTCCTCATCGACACT
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

FIG. 7 B

1150 1170 1190
TACTCCAGTAACTGCTGCTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCAGCCCTGT
TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys

1210 1230 1250
GTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTGTGGAGCCAAAGCCGACA
ValValAsnGluTyrTyrTyrArgLysLysCysGluSerIleValGluProLysProThr

1270 1290 1310
TTAAAGTATGTGTCCTTTGTGGATGAATCCACATTAGGATGGTGAACCAGCAGCTACTA
LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu

1330 1350 1370
GGGAGAAGTTTGCAAGATGTCAAGGGCCAAGAAGTCCCAAGACCTGCGATGGACTTCACA
GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr

1390 1410 1430
GATTTGTCCAGGCTGCCCCCTGGCCCTCCATGACACACCCCGATTCTGGACAACCAGAG
AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu

1450 1470 1490
GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCCGTCTGGTGC
GluIleGlnLeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys

1510 1530 1550
CAGTGTGGAAGATGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTG
GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluGluLeu

1570 1590 1610
TGCTGCCGGAAAAAGCCGGGGGCTGCATCACCACTCAGAGCTGTTTCAGGAAGCTGGTC
CysCysArgLysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuVal

1630 1650 1670
CTGTCCAGACACGTCTCTGCAGTTCTCTCTGCTCTACCAGGAGCCCTTGCTGGCGCTGGAT
LeuSerArgHisValLeuGlnPheLeuLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp

1690 1710 1730

FIG. 7 C

GTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGC
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750 1770 1790
TTCGGCTCCAGGACATGGCTGACTTTGCCATCCTGCCCAGCTGCTGCCGCTGGAGGATC
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810 1830 1850
CGGAAAGAGTTTCCAAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGC
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870 1890 1910
CAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCA

1930 1950 1970
CCTGAGATCGGGAGTTGGAGACCCGCTGGCTAACAAGGCGAAATCCTGTCTGTACTAAA

1990 2010 2030
AATACAAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050 2070 2090
GAGGCACAAGAATCACTTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110 2130 2150
CTGCTCTCCAGCCTGGGAGGCACAGCAAAGTGTCCCAAAAAAAAAAAAAAGAGTCCTTAC

2170 2190 2210
CAATAGCAGGGGCTGCAGTAGCCATGTTAACATGACATTACCAGCAACTTGAACCTCAC

2230 2250 2270
CTGCAAAGCTCTGTGGCCACATTTTCAGCCAAAGGGAAATATGCTTTCATCTTCTGTGTC

2290 2310 2330
TCTCTGTGTCTGAGAGCAAAGTGACCTGGTTAAACAAACCAGAATCCCTCTACATGGACT

2350 2370 2390

FIG. 7 D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCCTA

2410

2430

2450

GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTTGCCCCAACTACTATCTCAGAGATATTGT

2470

2490

2510

GAGGACAAATTGAGACAGTGCACATGAACTGTCTTTTAATGTGTAAAGATCTACATGAAT

2530

2550

2570

GCAAAACATTTTCATTATGAGGTCAGACTAGGATAATGTCCAACATAAAACAAACCCCTTTT

2590

2610

2630

CATCCTGGCTGGAGAATGTGGAGAACTAAAGGTGGCCACAAATTCTTTGACACTCAAGTC

2650

2670

2690

CCCCAAGACCTAAGGGTTTTATCTCCTCCCCTTGAATATGGGTGGCTCTGATTGCTTTAT

2710

2730

2750

CCAAAAGTGGAAGTGACATTGTGTCAGTTTCAGATCCTGATCTTAAGAGGCTGACAGCTT

2770

2790

2810

CTACTTGCTGTCCCTTGGAACCTTGCTATCGGGGAAGCCAGACGCCATTTAAAGTCTG

2830

2850

2870

CCTATCCTGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGACCAAGG

2890

2910

2930

CGGGCGGATCACTTAAAGTCAGGAGTCCAAGACCAGACTCGCCAACATGGTGAAACCGTA

2950

2970

2990

TCTCTAATAAAAAATACAAAAATTAGCTGGGCATGGTGCGGGCACCTGTAGTCCTAGCTAT

3010

3030

3050

CAAGAGGCTGAGACAGGAGAAACACTTGAACCTGGGAGGTGGAGGTTGCATTGAGCTGAG

FIG. 7 E

3070	3090	3110
ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAA		
3130	3150	3170
AAAAGAAAAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA		
3190	3210	3230
GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTCAAGCCATCCAAGCCCAGTCACCAAA		
3250	3270	3290
CATGAGAGAGAAGAAGCCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATACCGC		
3310	3330	3350
ATGATACATCCCAAGTGAGAACTGCCCCATAAATCCAGAAAACCACATTGCTATCTTAAG		
3370	3390	3410
TCCCTAAGTTTGGGGCTTATTTGTTCCACAGCAACAGGTAAGTGGAAACAGAGGGCAAGCC		
3430	3450	3470
TGATGAATGGGCACACAGACTCAGCCCATACTTCCCTGGTTCTAATGTTCTCAGGGAGC		
3490	3510	3530
CCGGACCAACCCTGGGAGCCTCAGGAAGTTAGGTTTCCACTGGACAGTTCTAGAAGGGCT		
3550	3570	3590
ATAGACCAAATCAGGTAAGTCAACAGACCAGCCTTGGAATCTATCAAATCTAACTGCTGA		
3610	3630	3650
GCTACCCAGTGCATTCCGATCCTCATCACAATTCTTTGACTGAAGGCCGGGCGTGGTGGC		
3670	3690	3710
TCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTCAGGA		

FIG. 7 F

3730 3750 3770
 GTTCGAGACCAGCCTGGCCAACATGGTGAGACCCTGTCTCTACTAAGAATACAAAAATTA
 3790 3810 3830
 GGTGGGGTGGCGGTGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATC
 3850 3870 3890
 TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCACTCCAGCCT
 3910 3930 3950
 AGATAACAGAGCAAGACTCTGTCTCAAAAAACAACAACAACAACAACAATTCTAT
 3970 3990 4010
 GACTGAAAGTGACTAAAAAGCTGGCTTTATGCCATTAACACTCTGTACTTTGCAGCCAAT
 4030 4050 4070
 CAGAACTGACGCAGTCTGGGTGCTAGCTGCTTCAAAGCAACCCACACCACACTTTTACC
 4090 4110 4130
 ATTTCCATACATCAACTGCTGAGAATATGAAAATGCACAGTGACAGGTTTTAGGATCCTG
 4150 4170 4190
 CTTCAGGATTTCTTTTCTGGTTTGGTCACTAGAGTTGGCTATTTATCTGTTTCTAAAC
 4210 4230 4250
 AATAGCTATTTTATCGAATAGTTTAGAGACCACTATTAAATATTGTGACTGATGAAGGAT
 4270 4290 4310
 CTGTGAATTTTTTTATATATGTTCTAAGAGTTACCATTTTGATACCTTTTAAAAACCAGC
 4330 4350 4370
 AGCTTTCTACTATATTCATGTAAAAACAGCATGAATAAAACCATTTTTTGATACAGGGTTT
 4390 4410 4430

FIG. 7 G

TATTTGGCTTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTTGATTTTACT

4450 4470 4490
ACCTTTTCAAAGATATTTTAAAAAGTGGATTACTACATATGATTTCTTTGGAGCTTACAT

4510 4530 4550
TTCTTTACTTCACGAATTCTATGTCAGTGTACAAGTTTCCATTCTGATGGCTTCTGGGC

4570 4590 4610
CTTTGTACCTTTGTTTTTGGTGCCTTATTCCTAGTATGTTTCTATCACCTTAATGAGGCC

4630 4650 4670
GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTTCCAT

4690 4710 4730
CACCTTCCCCACTGATGCTCTGGGCGAGAGAGTGATGTGTCACTTCAACTGTGTGTAATA

4750 4770 4790
TGTCAGACACGTCTACAATAACAGGCGTCATATTTGTATTATTTTGTAGTTTACTGTAGA

4810 4830 4850
AAATAATGTCACCGCCAAAGGTGATGAGAGTCACGTTTTGTAGGATCTGTTTTCTTATAC

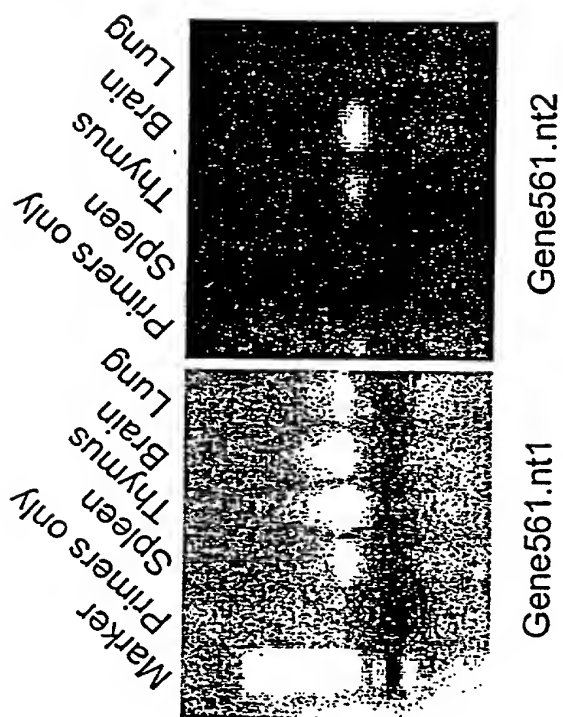
4870 4890 4910
TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTCATGGCTTCCTTTCTGTGTCAGA

4930 4950 4970
AGAGAAGGGATCTGCTTTCTCTTGGCTGATTTACATAGCATTGGTAATAGACATGCATT

4990 5010 5030
TCTCTTTCTAAAGGGGAGTAACTTTTTAAACCCTTCCTGATTTTAGCCTGGCAATGTAAG

5050 5070
TGTCTTAATGTGACTGTTTTGATAATTAAAAAAGGTATATAATTT

FIG. 7 H



RT/PCR of Gene561.nt1 and Gene561.nt2

FIG. 8

10 30 50
 TCGAAACAGCTGCCGGCTGGTCCCGGCCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCCGG
 70 90 110
 GCTGTGGGGGCGCCGCGAGCTGGGCGCGCCTCGGTGTGCCCGCGCCGCCAGCCCGCTCCA
 130 150 170
 GACGCGCCACCTGGGCGCTCCAAGAAGAGGCCGAAGTTTGCCGCGGCCGTGAGTTGGAGC
 190 210 230
 TCGCGCCGGGCGCGCTGCGCCGGGAGCTCCGGGGGCTTCCCTCGCTTCCCGGTATTGTTTG
 250 270 290
 CAAACTTTGCTGCTCTCCGCCGCGGCCCCCAACTCGGCGGACGCCGGGCGCGGAGAGCCG
 310 330 350
 AGCCGGGGGCGCTGTGCGCAGCGCTCGGGCCAGGCCGGGCGGGCATGGGCGGGGGCCCCGA
 370 390 410
 GCAGGGGTGGAGAGCCGGGGCCAGCAGCAGCCCGTGCCCGGGAGCGGCGGCGCTGAGGGG
 430 450 470
 CGCGGAGCTCCCCGCGAGGACACGTCCAACGCCAGCATGCAGCGCCCGGGCCCCCGCCTG
 MetGlnArgProGlyProArgLeu
 490 510 530
 TGGCTGGTCTCTGCAGGTGATGGGCTCGTGCGCCGCCATCAGCTCCATGGACATGGAGCGC
 TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg
 550 570 590
 CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCCGATGTGCAAGGACATCGGCTACAAC
 ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn
 610 630 650

FIG. 9 A

ATGACTCGTATGCCCAACCTGATGGGCCACGAGAACCAGCGAGGCAGCCATCCAGTTG
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670 690 710
CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGGCCACCTCCGCTTCTTCTGTGC
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730 750 770
TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCCGCTGCCGGGTC
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790 810 830
ATGTGCGAGCAGGCCCGGCTCAAGTGCTCCCCGATTATGGAGCAGTTCAACTTCAAGTGG
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850 870 890
CCCGACTCCCTGGACTGCCGGAACCTCCCCAACAAGAACGACCCCAACTACCTGTGCATG
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910 930 950
GAGGCGCCCAACAACGGCTCGGACGAGCCCACCGGGGCTCGGGCCTGTTCCCGCCGCTG
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970 990 1010
TTCCGGCCGCAGCGGCCCCACAGCGCGCAGGAGCACCCGCTGAAGGACGGGGGCCCCGGG
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030 1050 1070
CGCGCGGGCTGCGACAACCCGGGCAAGTTCCACCACGTGGAGAAGAGCGCGTCGTGCGCG
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090 1110 1130
CCGCTCTGCACGCCCGGCGTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGCAGTG
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150 1170 1190

FIG. 9 B

GTCTGGCTGGCCATCTGGGCGGTGCTGTGCTTCTTCTCCAGCGCCTTCACCGTGCTCACC
ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210 1230 1250
TTCCTCATCGACCCGGCCCGCTTCCGCTACCCGAGCGCCCATCATCTTCCTCTCCATG
PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270 1290 1310
TGCTACTGCGTCTACTCCGTGGGCTACCTCATCCGCCTCTTCGCCGGCGCCGAGAGCATC
CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330 1350 1370
GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGACTGGAGAGCACCGGC
AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390 1410 1430
TGCACGCTGGTCTTCTCGGTCTTCTACTTTCGGCATGGCCAGCTCGTGTGGTGGGTG
CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450 1470 1490
GTCCTCACGCTCACCTGGTTCCTGGCCGCCGGCAAGAAGTGGGGCCACGAGGCCATCGAA
ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510 1530 1550
GCCAACAGCAGCTACTTCCACCTGGCAGCCTGGGCCATCCCGCGGTGAAGACCATCCTG
AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570 1590 1610
ATCCTGGTCAATGCGCAGGGTGGCGGGGGACGAGCTCACCGGGGTCTGCTACGTGGGCAGC
IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630 1650 1670
ATGGACGTCAACGCGCTCACC GGCTTCGTGCTCATTCCCCTGGCCTGCTACCTGGTCATC
MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690 1710 1730

FIG. 9 C

GGCACGTCCTTCATCCTCTCGGGCTTCGTGGCCCTGTTCCACATCCGGAGGGTGATGAAG
GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

1750

1770

1790

ACGGGCGGCGAGAACACGGACAAGCTGGAGAAGCTCATGGTGCGTATCGGGCTCTTCTCT
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer

1810

1830

1850

GTGCTGTACACCGTGCCGGCCACCTGTGTGATCGCCTGCTACTTTTACGAACGCCTCAAC
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn

1870

1890

1910

ATGGATTACTGGAAGATCCTGGCGGCGCAGCACAAAGTGCAAAATGAACAACCAGACTAA
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys

1930

1950

1970

ACGCTGGACTGCCTGATGGCCGCTCCATCCCCGCCGTGGAGATCTTCATGGTGAAGATC
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle

1990

2010

2030

TTTATGCTGCTGGTGGTGGGGATCACCAGCGGGATGTGGATTGACCTCCAAGACTCTG
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu

2050

2070

2090

CAGTCCTGGCAGCAGGTGTGCAGCCGTAGGTTAAAGAAGAAGAGCCGGAGAAAACCGGCC
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysLysSerArgArgLysProAla

2110

2130

2150

AGCGTGATCACCAGCGGTGGGATTTACAAAAAGCCCAGCATCCCAGAAAACCTACCAC
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis

2170

2190

2210

GGGAAATATGAGATCCCTGCCCAGTCGCCACCTGCGTGTGAACAGGGCTGGAGGGAAGG
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd

2230

2250

2270

FIG. 9 D

GCACAGGGGCGCCCGGAGCTAAGATGTGGTGCTTTTCTTGTTGTGTTTTCTTTCTTCT

2290

2310

2330

TCTTCTTTTTTTTTTTTTTATAAAAGCAAAAGAGAAATACATAAAAAGTGTTTACCCTG

2350

2370

2390

AAATTCAGGATGCTGTGATACACTGAAAGGAAAAATGTACTTAAAGGGTTTGTGTTTGT

2410

2430

2450

TTGGTTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTCTTGTTGTAACATAATTGT

2470

2490

2510

GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAAACCTTTGTTTAGAGCCCTCCSTAAATAT

2530

2550

2570

ACATCTGTGTATTTGAGTTGGCTTTGCTACCCATTACAAATAAGAGGACAGATAACTGC

2590

2610

2630

TTTGCAAATTCAGAGCCTCCCTGGGTTAACAAATGAGCCATCCCCAGGGCCCCACCCCC

2650

2670

2690

AGGAAGGCCACAGTGCTGGGCGGCATCCCTGCAGAGGAAAGACAGGACCCGGGGCCCGCC

2710

2730

2750

TCACACCCCAGTGGATTTGGAGTTGCTTAAATAGACTCCGGCCTTCACCAATAGTCTCT

2770

2790

2810

CTGCAAGACAGAAACCTCCATCAAACCTCACATTTGTGAACTCAAACGATGTGCAATACA

2830

2850

2870

TTTTTTTCTCTTCTTGAAAATAAAAAGAGAAACAAGTATTTGCTATATATAAAGACA

2890

2910

2930

FIG. 9 E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCCGCCCTCAGAAACCCCTTCAGTGC

2950

2970

2990

TACATTTTGTGGCTTTTAAATGGAAACCAAGCCAATGTTATAGACGTTTGGACTGATTG

3010

3030

3050

TGGAAAGGAGGGGGGAAGAGGGAGAAGGATCATTCAAAGTTACCCAAAGGGCTTATTGA

3070

3090

3110

CTCTTTCTATTGTTAAACAAATGATTTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG

3130

3150

3170

AGACACTTTGTCTAGTGTATTCTCTTCACAGTGCCAGGAAAGAGTGGTTTCTGCGTGTGT

3190

3210

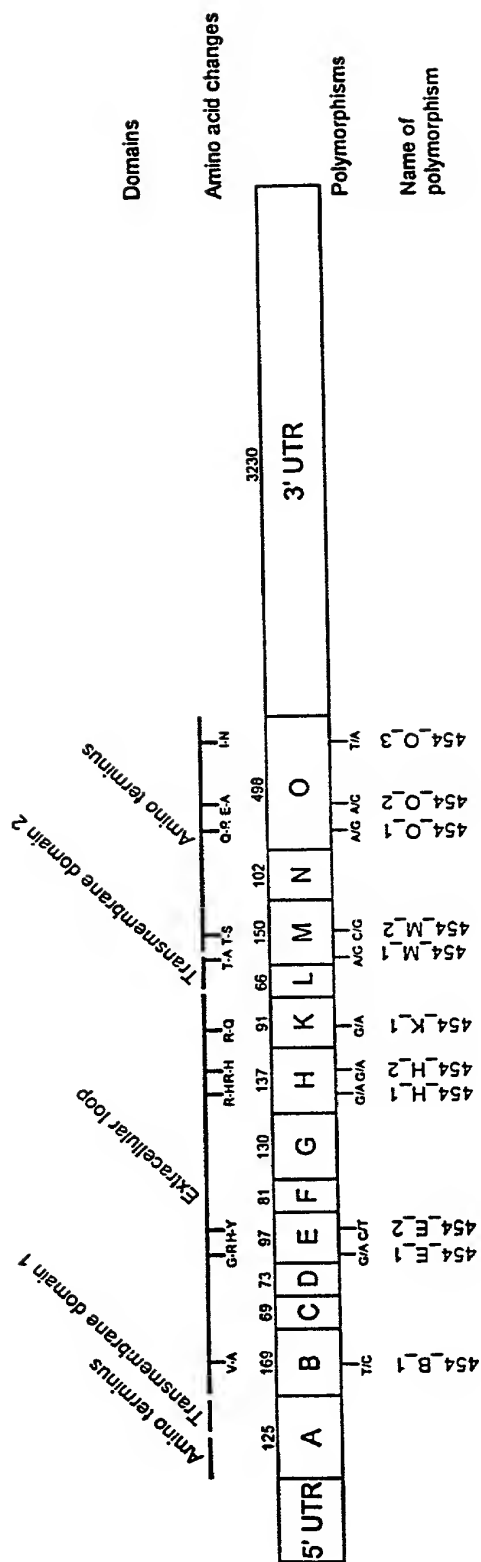
3230

ATATTTGTAATATATGATAATTTTCATGCTCCACTATTTTATTAAAAATAAAATATGTTT

3250

TTTAGTTTGCTGCT

FIG. 9 F



Location of SNPs/Amino Acid Changes/Domain within the Transcript of Gene 454

FIG. 10

Chr. 12 Case(Asthma)/Control: Alleles

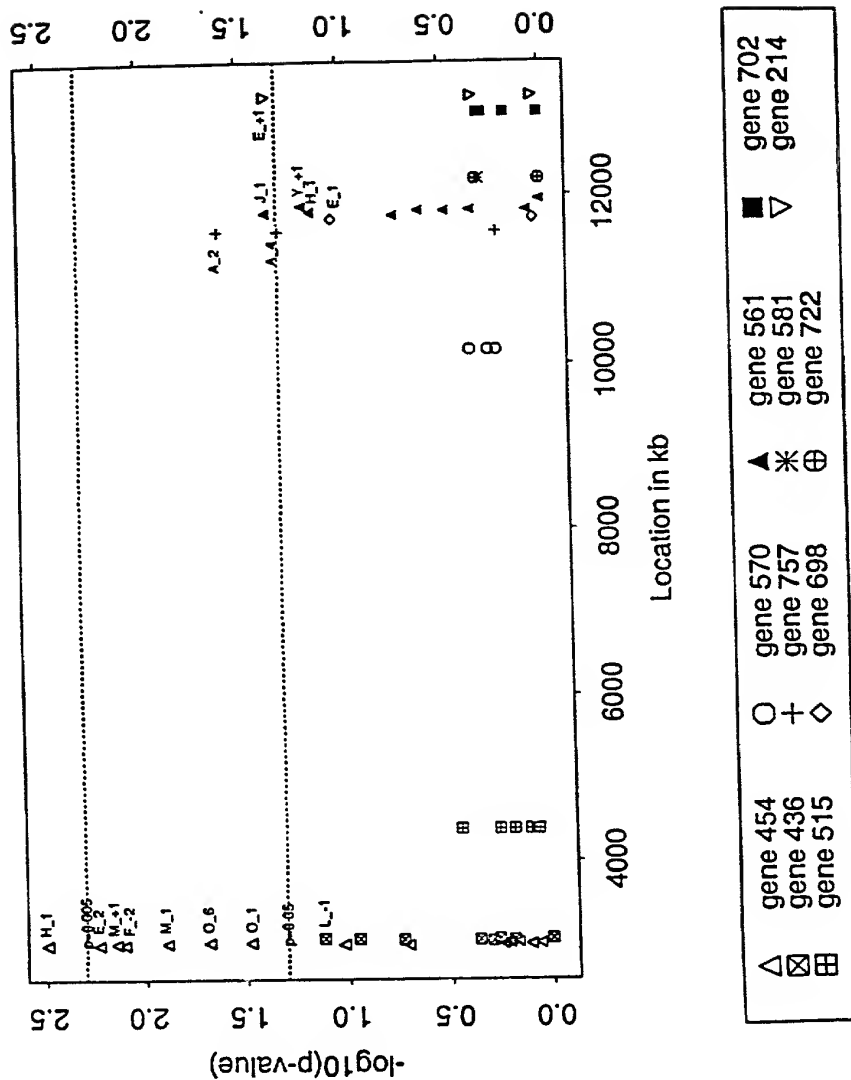


FIG. 11

Chr. 12 Case(Asthma)/Control: Alleles

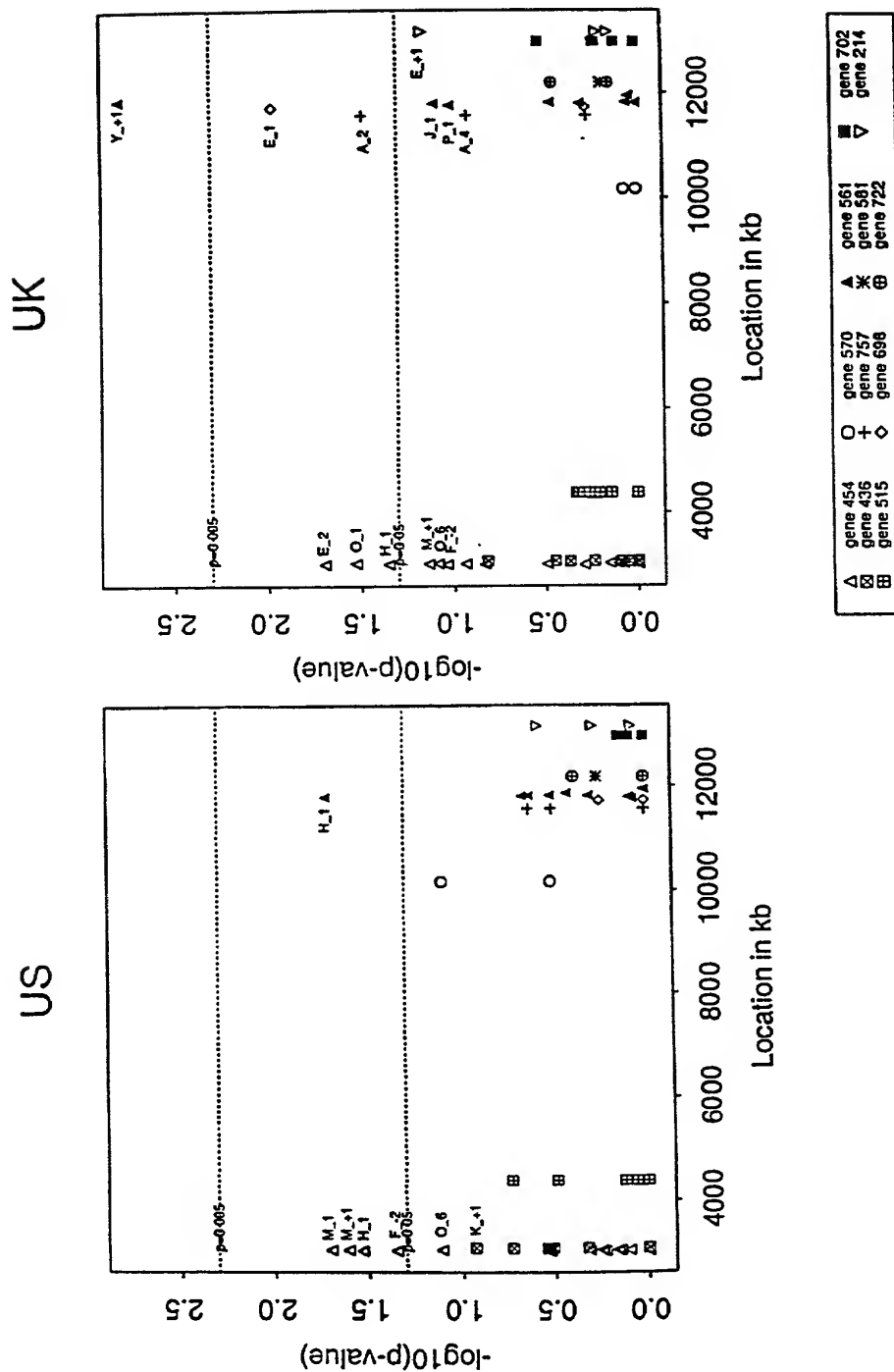
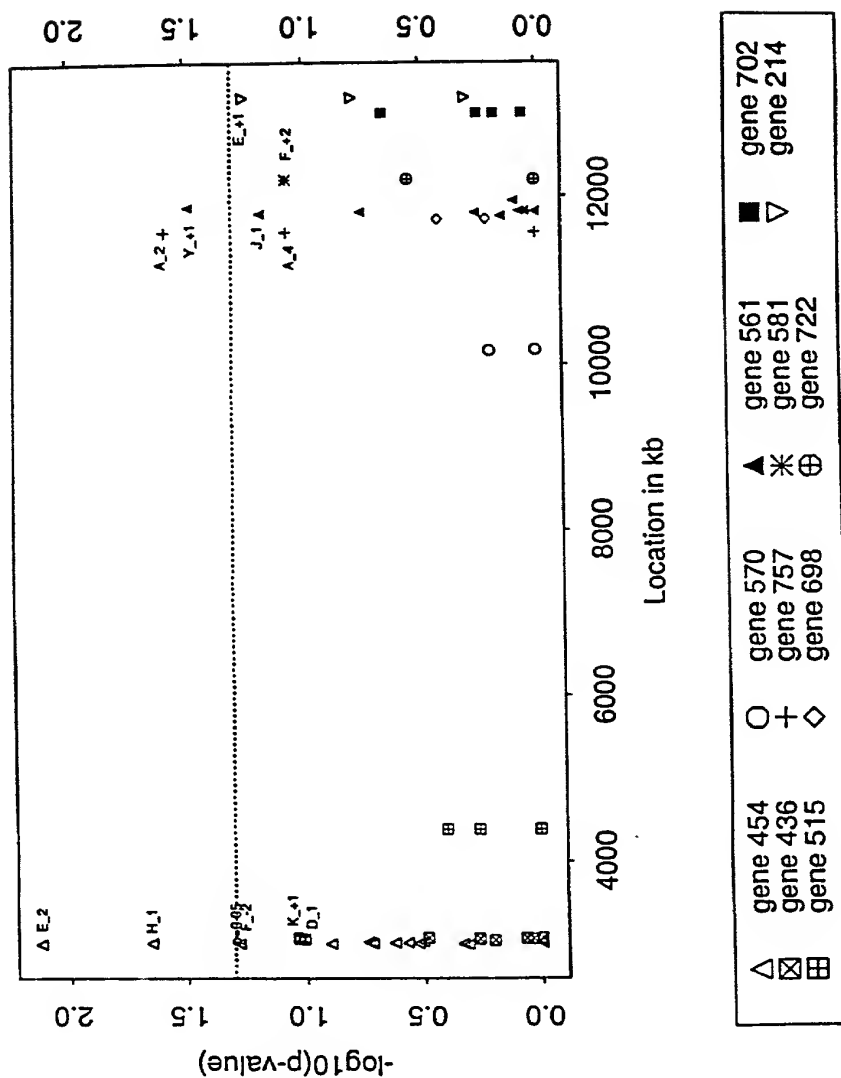
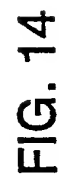


FIG. 12

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles





Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

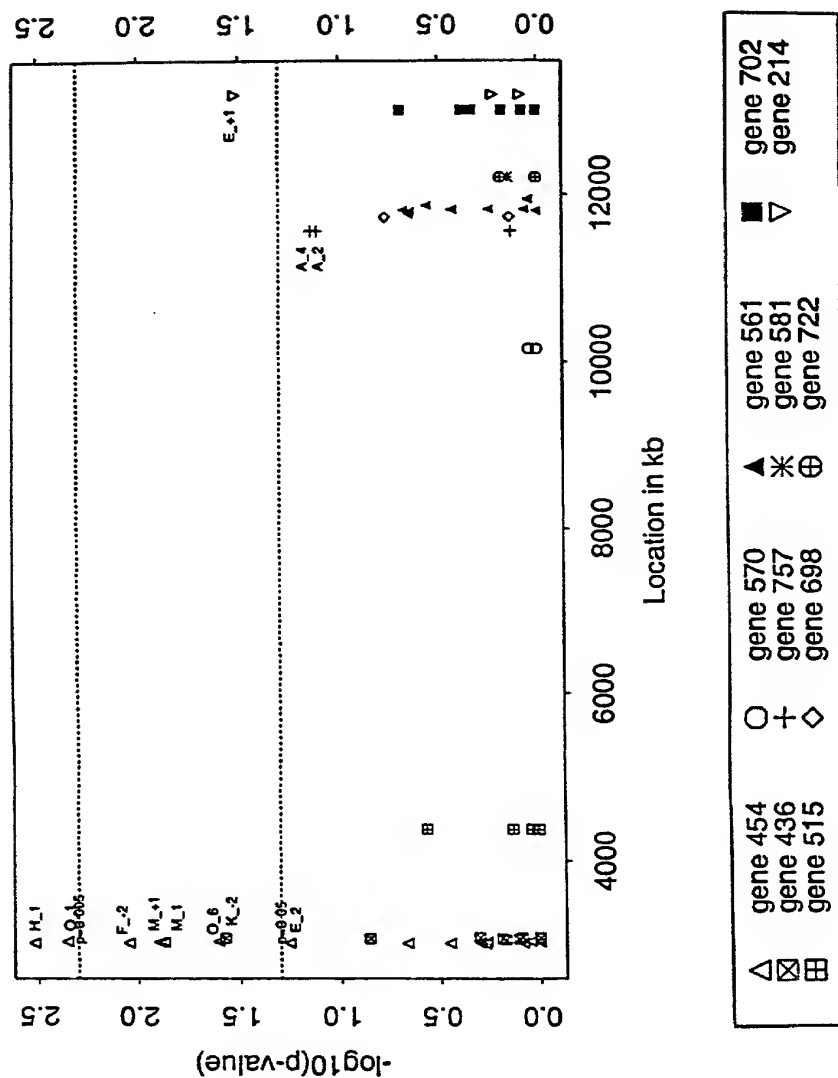


FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

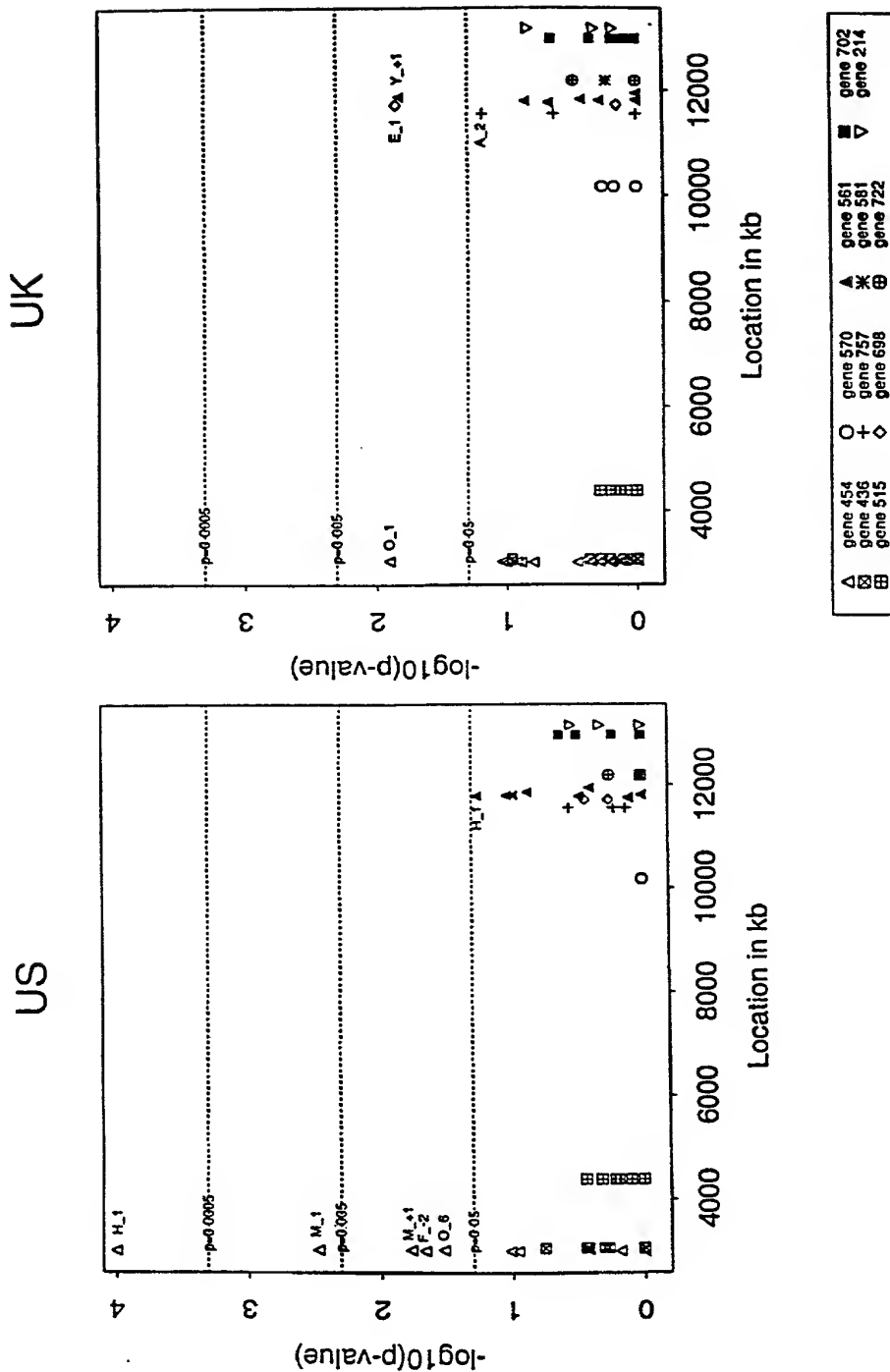


FIG. 16

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

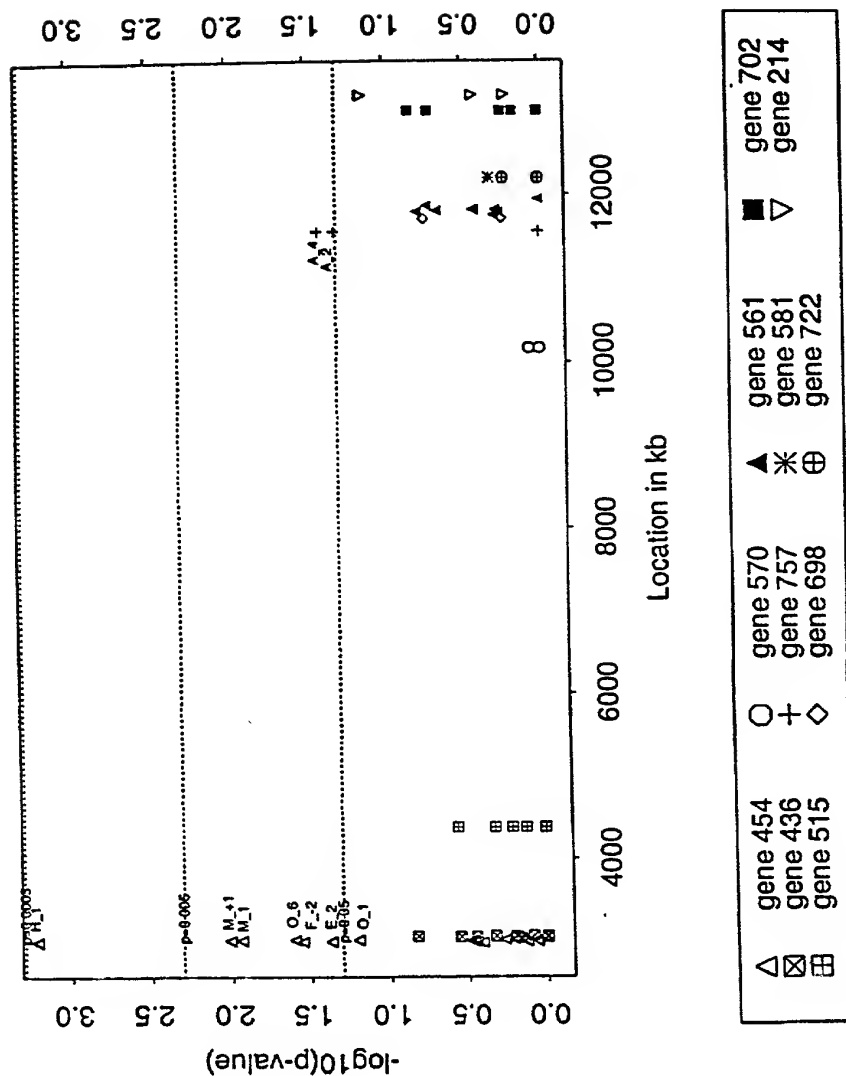
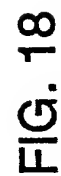


FIG. 17



Chr. 12 Case(Asthma)/Control: Haplotype

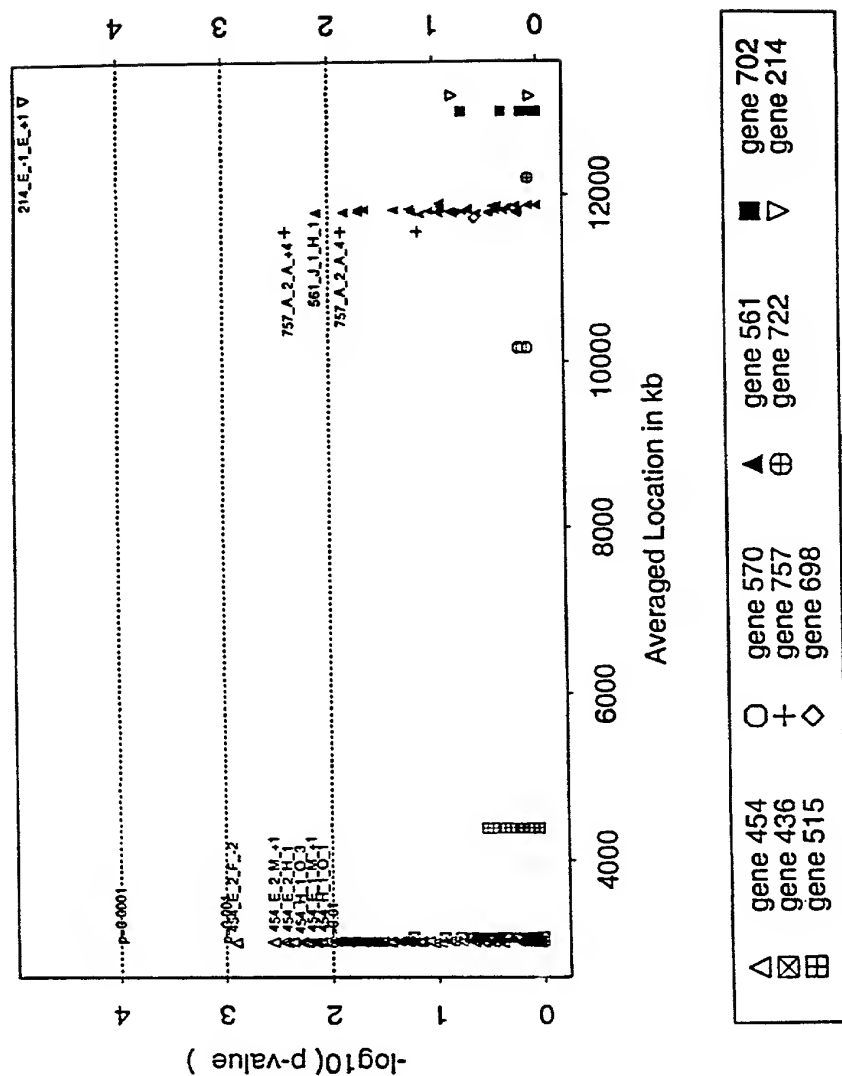


FIG. 19

Chr. 12 Case(Asthma)/Control: Haplotype

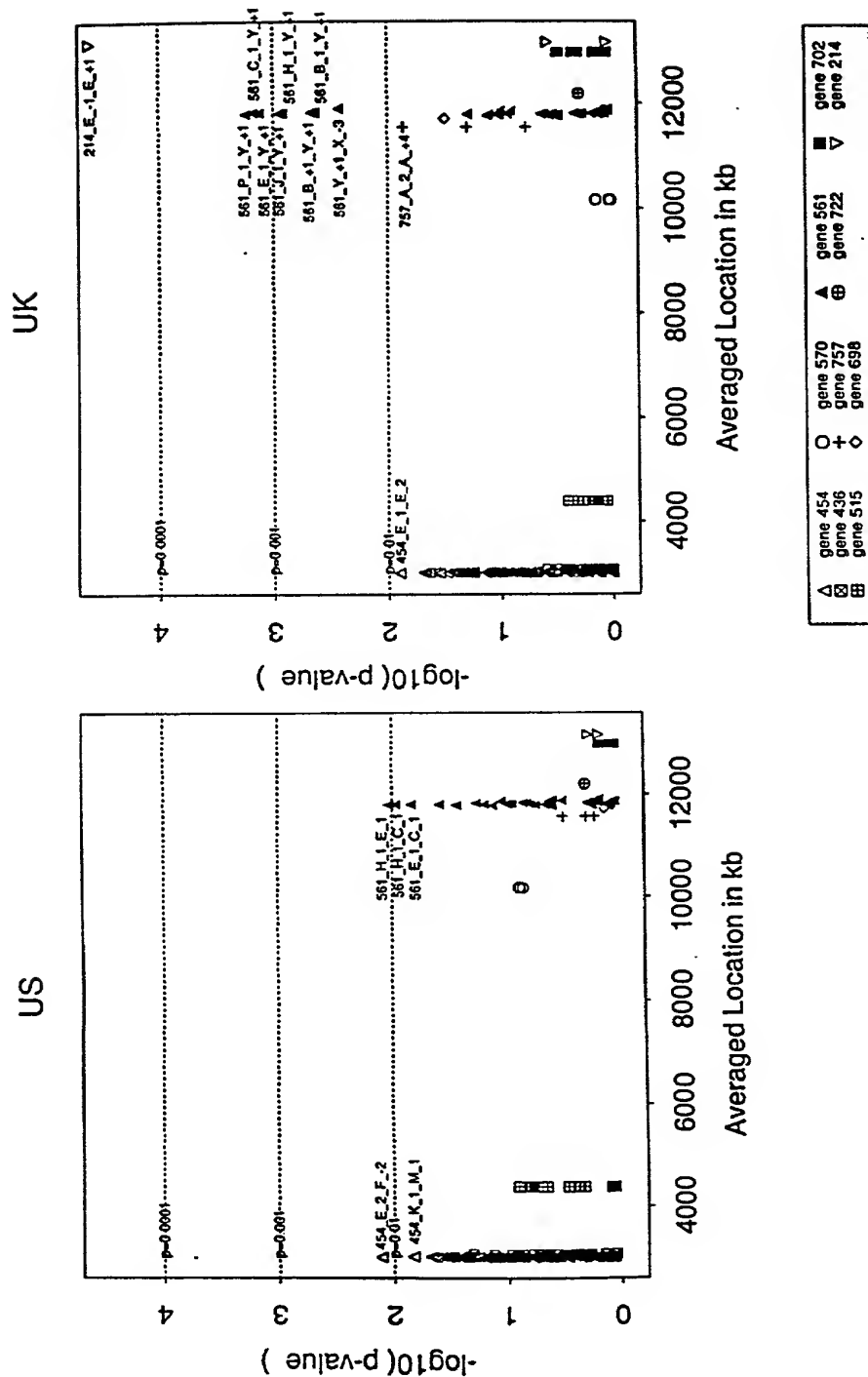


FIG. 20

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

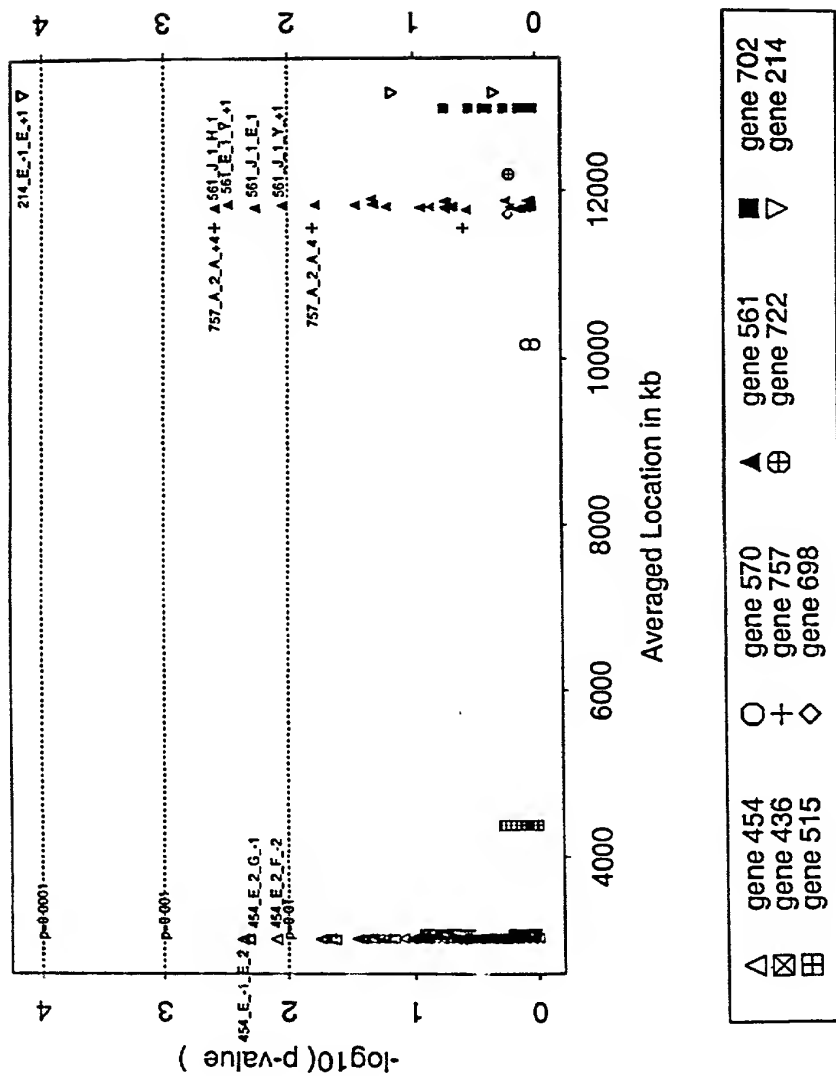


FIG. 21

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

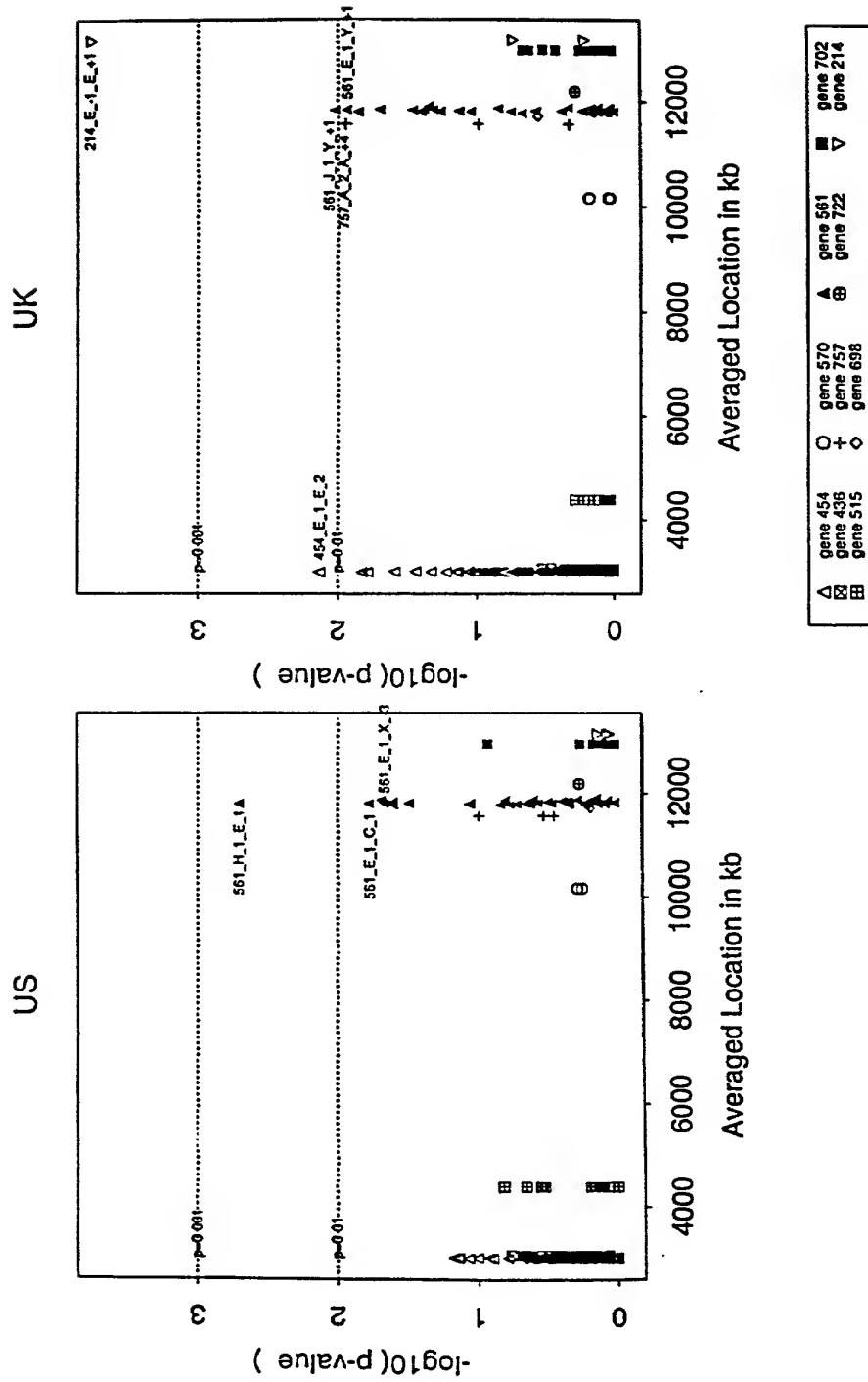


FIG. 22

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

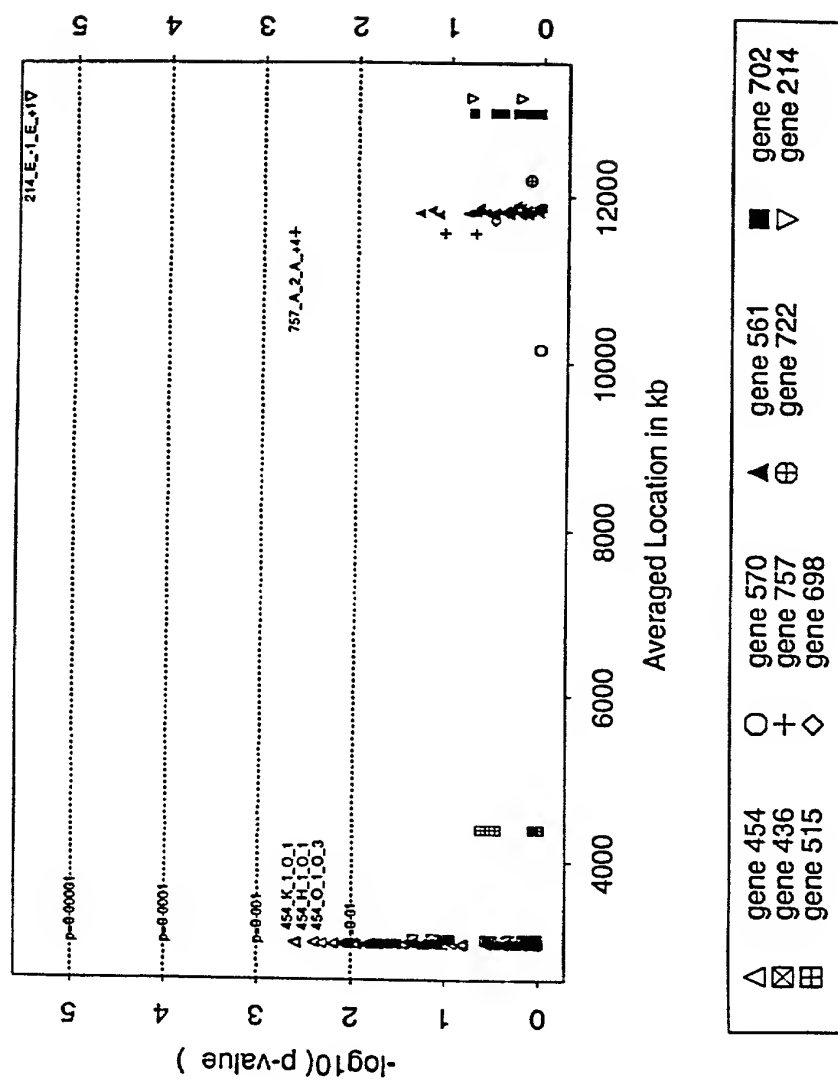


FIG. 23

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

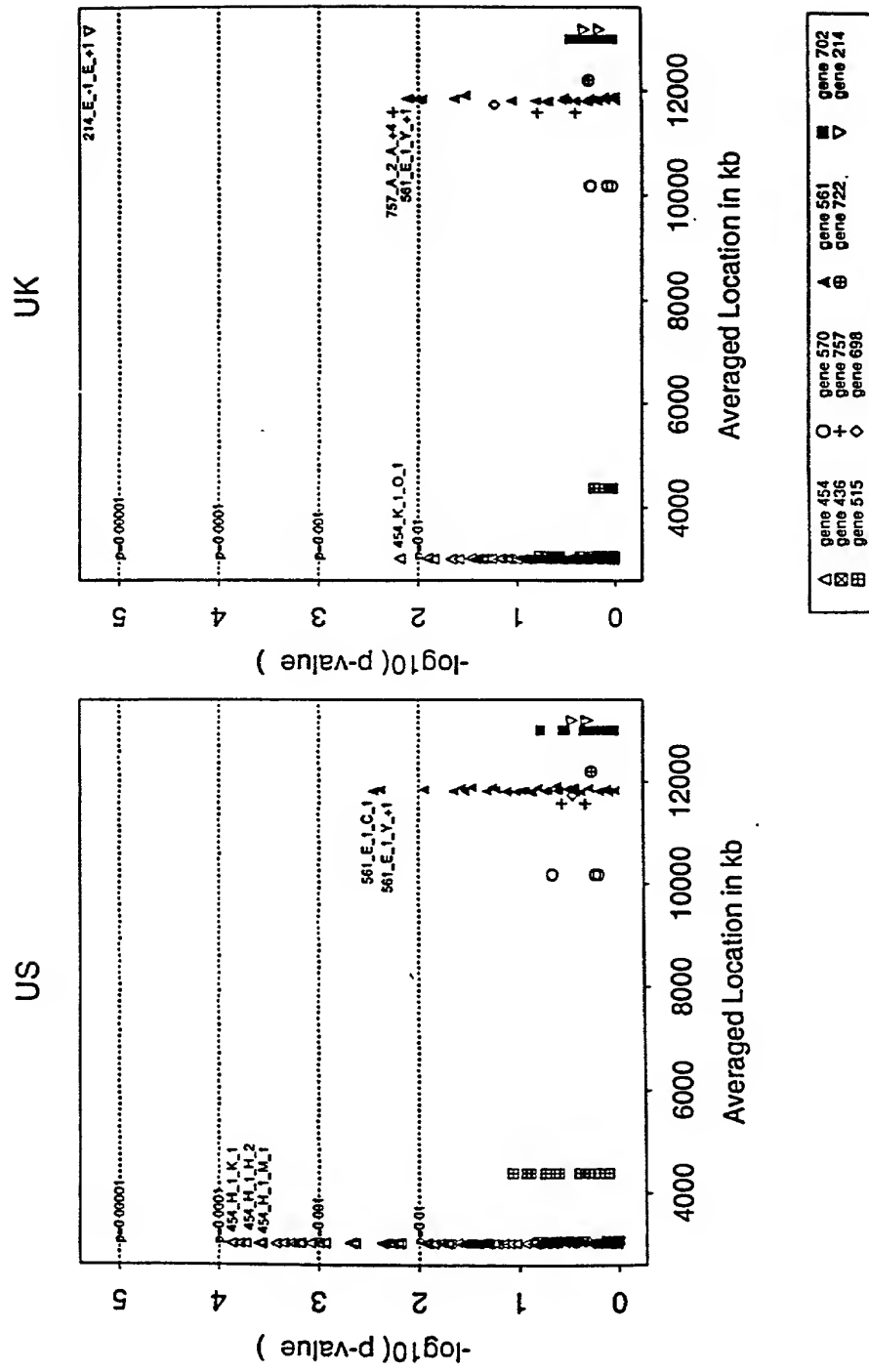


FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

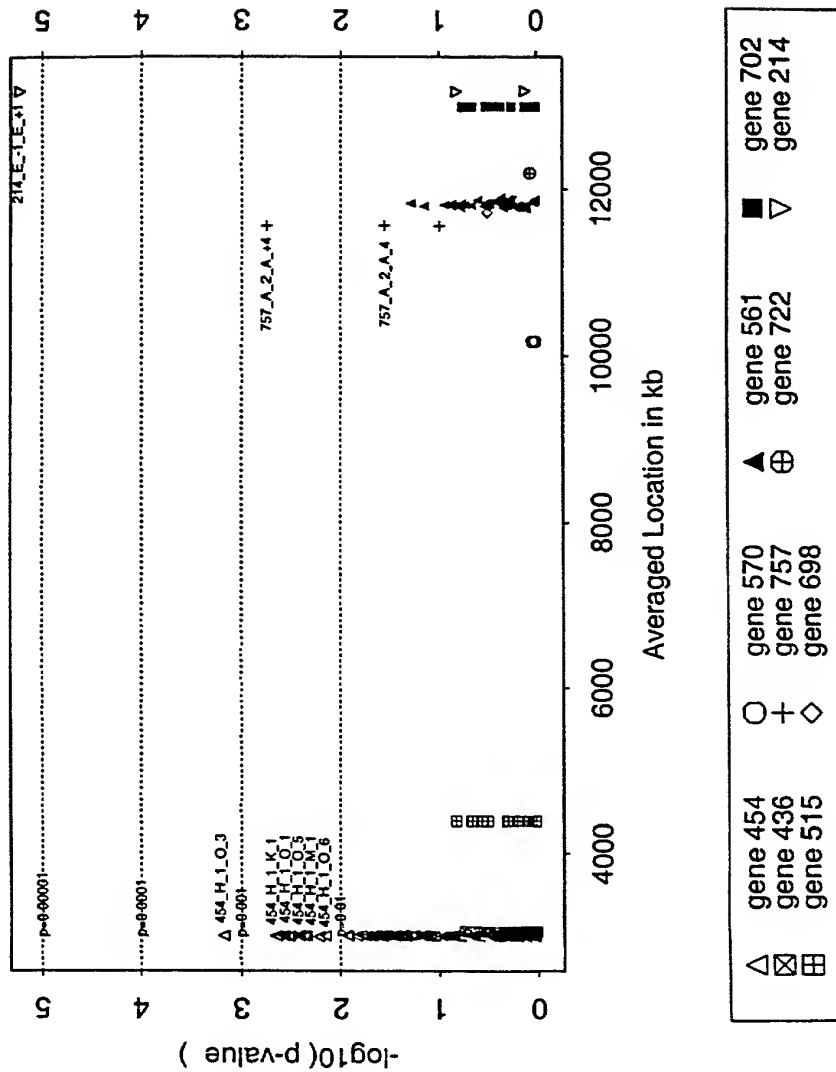


FIG. 25

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

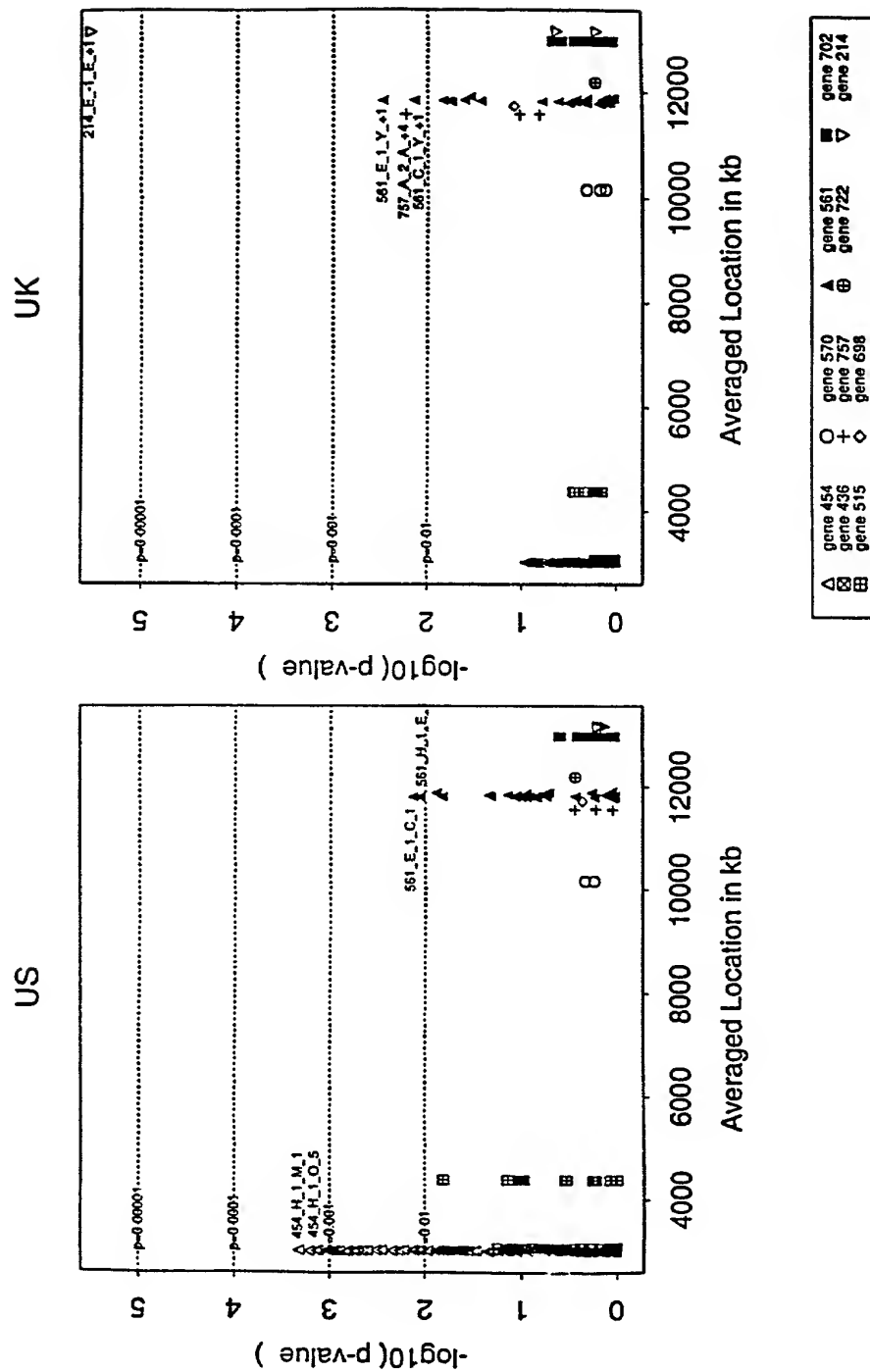


FIG. 26

10 30 50
 CTTGGAATGACCCGCCACCTGAAGCCTGCAGGTGCTGAGGCCACATTCGATCAGACC
 70 90 110
 CAAGCTTTGGGAGACCGCTGGGGAAATTTCCCACTTCTCTCCTGAGACCAGGAACTCAG
 130 150 170
 CAGAGAACTTTGTGGAAAATGAACTGAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA
 190 210 230
 TCCCATCATGCAGGCCTTCCCACAAGGGCCCGGCAGCATGACAAGGTGAAGGCAGAGTAT
 250 270 290
 GTGCATCTCAACCAYCCGCTCACCCCTCGTGACCAGAGAGCGCGATTGGCCGTGAAGGAG
 310 330 350
 AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCCTGAAGCATATGCGAGAG
 MetArgGlu
 370 390 410
 GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT
 AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer
 430 450 470
 GCCAAGCAGCAGGAAATTGACCTTCTGCAGAAGTCCAAGGTTGAGAGCTGGAAGAGAAA
 AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluGluLys
 490 510 530
 TGCCGGAAGTCAAAGTGAGCAGTTCAACCTGCTGTCCCGGGACCTGGAGAAGTTCCGGCAG
 CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln
 550 570 590
 CACGCTGGCAAGATTGACCTGCTGGGTGGCAGCGCGGTGGCCCCCTGGACATCTCCACG
 HisAlaGlyLysIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr

FIG. 27 A

610	630	650
G C C C C C A G C A A G C C T T T C C C A C A G T T C A T G A A T G G C C T A G C C A C C T C C C T C G G C A A A G G T AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly		
670	690	710
C A G G A G A G C G C T A T T G G A G G C A G C T C T G C G A T C G G T G A A T A T A T C C G G C C C T T C C G C A G GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln		
730	750	770
C C T G G T G A C A G G C C G G A G C C T C T G T C C G C C A A G C C C A C C T T C C T G T C G A G A T C C G G T A G C ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer		
790	810	830
G C A A G A T G C A G A T C T G A G T C A G A C A T G G A G A A T G A A C G G A A T T C C A A T A C C T C C A A G C A G AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln		
850	870	890
A G A T A C T C G G G G A A G G T C C A C C T C T G T G T T G C C G C T A T A G T T A C A A C C C C T T C G A T G G A ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly		
910	930	950
C C G A A C G A G A A C C C G A A G C T G A G C T G C C C C T C A C G G C G G G A A A A T A C C T C T A C G T C T A T ProAsnGluAsnProGluAlaGluLeuProLeuThr <u>Ala</u> GlyLysTyrLeuTyrValTyr		
970	990	1010
G G A G A C A T G G A T G A G G A T G G G T T C T A T G A A G G A G A G C T C C T C G A T G G C C A G A G G G T C T G GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu		
1030	1050	1070
G T G C C C T C C A A C T T C G T G G A C T T T G T G C A G G A C A A C G A G T C G C G G T T G G C A A G C A C G C T G ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu		
1090	1110	1130
G G G A A C G A G C A G G A T C A G A A C T T C A T C A A C C A T T C C G G C A T C G G C C T G G A G G G A G A G C A C GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis		
1150	1170	1190
A T C C T G G A C C T C C A C T C C C C A A C C C A C A T A G A T G C G G G C A T C A C C G A C A A C A G T G C C G G G		

FIG. 27 B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210 1230 1250
ACCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCTAGAAAAATC
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270 1290 1310
ACCCTCATCAAACAACTCGCCAAAAGTGTTATTGTGGGCTGGGAGCCCCGGCGGTGCCA
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330 1350 1370
CCAGGATGGGGAACGGTGAGCAGCTACAACGTCCTGGTGACAAGGAGACACGCATGAAC
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390 1410 1430
CTCACGCTGGGGAGCAGAACTAAAGCCCTCATCGAGAAGCTCAACATGGCAGCCTGCACC
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450 1470 1490
TACCGCATCTCCGTGCAGTGCCTCACCAGCAGGGGCAGCTCGGATGAGCTGCAGTGCACG
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510 1530 1550
CTGCTGGTGGGCAAGGACGTGGTGGTGGCCCCCTCCACCTGCGGGTGGACAACATCACG
LeuLeuValGlyLysAspValValValAlaProSerHisLeuArgValAspAsnIleThr

1570 1590 1610
CAGATCTCCGCCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCATCTTC
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630 1650 1670
CTCAACGAGGAGGAGTTCGACATCGTCAAGGCCGCCAGGTACAAGTACCAGTTCTTCAAT
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690 1710 1730
CTCAGGCCCAACATGGCCTATAAGGTGAAGTTCTGGCCAAACCCACCAGATGCCGTGG
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

FIG. 27 C

1750 1770 1790
 CAGCTCCCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTTGTGGAGTTCTCCACGTTGCCT
 GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro

1810 1830 1850
 GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGGTGACCCCCGCCACC
 AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr

1870 1890 1910
 ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCCACGGGCTGTCCAATGGCGCAAAC
 IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn

1930 1950 1970
 GTTACCGGCTACGGCGTGATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG
 ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr

1990 2010 2030
 GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC
 AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr

2050 2070 2090
 GTGCGGACCTCTCCGCCCAGGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTTCCCCC
 ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro

2110 2130 2150
 GAGCTCCTGGTGCTCCTACCCCCACCCGAGACCTGCACCCCAATCAAAGCCATTAGCA
 GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla

2170 2190 2210
 AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGATGGATGAG
 SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu

2230 2250 2270
 GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGCCGCCCGTG
 AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal

2290 2310 2330
 GGCCCCGGAAGGCGGTGCGCCTCACCCAGCCGCATCCTGCCGAGCCACAGGGCACCCCCG

FIG. 27 D

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350

2370

2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCCGAGAGC
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410

2430

2450

AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470

2490

2510

TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530

2550

2570

GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGCCGCACTGTTGCCATGGAGACGAGTAC
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590

2610

2630

CACACAGAGAGCAGCCGGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGluGlu

2650

2670

2690

CTGTATTCTGAAATGCAGCTGGAAGATGGGGGAAGGAGCGGCCAGCGGCACGTCCCAC
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710

2730

2750

AATGCCCTCAAGATTTTAGGGAACCCAGCCTCTGCAGGACGGGTGGATCACATGGGCCGG
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770

2790

2810

AGGTTTCCCCGTGGCAGCGCTGGTCCTCAGAGTCCCGGCCCGTGACAGTCCCATCCATC
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830

2850

2870

GACGATTACGGGCGAGACCGCCTTTCTCCAGACTTCTATGAAGAGTCAGAACTGACCCCT
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

FIG. 27 E

2890	2910	2930
GGTGCCGAAGAGCTCCCGGCCCGGATCTTTGTGGCTCTCTTTGACTACGACCCGCTCACC		
GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr		
2950	2970	2990
ATGTCCCAAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTTAAAGAAGGCCAGATCATC		
MetSerProAsnProAspAlaAlaGluGluGluLeuProPheLysGluGlyGlnIleIle		
3010	3030	3050
AAGGTTTATGGTGATAAAGACGCTGATGGATTCTACCGTGGGGAAACCTGTGCCCGGCTT		
LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu		
3070	3090	3110
GGCCTTATTCCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGATGGAT		
GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp		
3130	3150	3170
CAGCTTCTTAGACAGGGCTTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAGC		
GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer		
3190	3210	3230
AGGAGAAGTGGCAGGCGTCATTCGGTATCGACGCGGAGAATGGTGGCCCTGTATGACTAC		
ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr		
3250	3270	3290
GACCCAGAGAAAGCTCGCCCAACGTCGATGTCGAGGCCGAACCTTACATTTGCACAGGA		
AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly		
3310	3330	3350
GATATTATTACAGTTTTTGGTGAAATTGATGAAGATGGATTTTATTATGGGGAGCTGAAC		
AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn		
3370	3390	3410
GGGCAGAAAGGCCTTGTGCCCTCAAACCTTCTTGAAGAAGTGCCTGATGACGTAGAAGTC		
GlyGlnLysGlyLeuValProSerAsnPheLeuGluGluValProAspAspValGluVal		
3430	3450	3470
TATCTTTCTGATGCTCCATCCCACTACTCTCAAGATACGCCAATGCGCTCAAAGGCAAAA		

FIG. 27 F

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490 3510 3530
AGGAAGAAGAGTGTTCATTTTCATACCTTAATCAGGCAATGTAGCCTTCACGTAAGTGAGC
ArgLysLysSerValHisPheIleProEnd

3550 3570 3590
AACTGAAGATACCGATAAAGATACCAACTTAAGCTACCTTAACCGGGCCAGTGTGGTAGA

3610 3630 3650
CTTAAGGCTTCATTGTGGGGTTAAAAAAGATACAAAGAAATATGTCTCAAAA

3670 3690 3710
ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAAGCAACTGAATTTA

3730 3750 3770
TAGTGAAGCAAATCATCTTTAATAATCATTTCTACTATTTGCATTAAAGAATATTTGAAA

3790 3810 3830
GGCCAACATTGGGAACATATTTCTTAACAAGCTAACTGTGTGTTTACATAGAGAGAGCTG

3850 3870 3890
CATATTGCATTGTTAGCCACTCTTGGAAAAAGCACAACTAACAACATGTTTACTATAG

3910 3930 3950
GAAGCTTTACTTTAGAAACTTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970 3990 4010
CGAGTGTTGGCTCTGAACACTCCAACACTGGCTCGAGTGGCCAGAACGTGTTTTCTTA

4030 4050 4070
AGTAACCCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCCTCAAAGCACAAATCATCCTG

4090 4110 4130
TGACAGAAGTTGCTGCAACACGCGTTTGTGTTGGTATACCAATGCAATACTAAGTTGAT

FIG. 27 G

4150 4170 4190
 GAAGCAGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTTCAGGTGTACTTT
 4210 4230 4250
 GGGATGCTTTACTAGGTGTTTTCCATTAGAATTAGACCTTGATTTTAAATCCAAGCAAGC
 4270 4290 4310
 TTGAAGCCCCTTGGCTTACAGCATTTGCCTGCTGAATACTAAACACTCACATGGCAAGAG
 4330 4350 4370
 TTGCTCTGGAGAGGTAGGGCCAGAGGAATGCTGCTGCACTGCCAACTCAGGCACATGCTT
 4390 4410 4430
 AGCTGTAAAGGGAAGCGAGGTGAAGTCGTCCTGCAGCGTATTAGAGTAAAAGTCTACCCC
 4450 4470 4490
 TCTGAAGCACTATTAAGCGCTTAACGTATATTTAAATACTACCATGTGCTATCTACTGAG
 4510 4530 4550
 GAAGATTCATGTTCAATTATTTGGAAATAATGCAAGCATCCACTAAGGGCCTTTAAGCTT
 4570 4590 4610
 TCTTTGATTATAATTAAGGTTCATTTTAGTTTTTTTTTTTTCTTTCAACCAGTGTGCCAT
 4630 4650 4670
 CTCCAATATTTCTATAGTATACCAACCACCCCAGGAATGCACTTTAACAATATCAGGATT
 4690 4710 4730
 TTATATAACCAAATAGTTTCAAATACAACAAAATTCCTTTATGAACTTTGCTTTTTAA
 4750 4770 4790
 GACTACTGATGGGTACTCGGCCAACTTTACTATCAACCTAATTCAGATCATGTCTCCCC

FIG. 27 H

4810 4830 4850
 T G C C C T T A G T C T T C A T T T A T G A A G T G A A T T A T T A C C T G C C T T A G C T T T G C C A A G C A A C G
 4870 4890 4910
 G C C A C C C C G C A C T C C C T C G A G A C A G A G A A C G G A A C C C A C A C A T T T A T G T C T G G G G C C T C
 4930 4950 4970
 T C T C T G G C G T G C T G T G G G A G A G A C C T T T G C T T C T A T G G C A T A C T T C A A C A A C T G A A A G
 4990 5010 5030
 A A C A A T G A A C C C C C T G A C C T T T C C T G G T G G G A A C G G G A C A G T A C G A T G T T A C C A A G
 5050 5070 5090
 T G A A T T C T G T T G T T G G C G C T C A C A C A C T C A A T A A A C T G T A A C A C T G T A C C T A C T A G G T T C
 5110 5130 5150
 C T C C T G A G G G T T C A G G T A C A G C A A G G A G A G C T C C A T C C C C C A C A G T C C A T C T C C A T T C G G
 5170 5190 5210
 G G T C A C C T A C G T C A T C T A T G G G T T C T G G T A G T C C T G G G A G A G G C A G G G A A T G T C C T C G A
 5230 5250 5270
 A A A A G A A A A G G G G C T G C T T T C C A A G G C A A G A A A C T G C T G A A A A A G C T G G G T G C A G T G A
 5290 5310 5330
 A A T G A T T C A T G T G C T T C C G G A C A A C T G C C A A T C T A T G T A A T T T T C T T T A A T T C C A A A C T
 5350 5370 5390
 A G G G C T T T C A T G A C T C A A G T A C T T C C T A A A A A A C C C A A T C T T C T C C C C T G A C A C C A G T A
 5410 5430 5450
 G A G A A T G C A C T T T T G C A C T A C C A A C C A C T T T A A C C A A C C A C G A G A A C A A A G A G G A G C G
 5470 5490 5510

FIG. 27 I

GTTGCTCTCTGTCACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTTGGGAGGTG

5530

5550

5570

GGAGGGGACGTCTTATTAACAAACGGGGGCGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590

5610

5630

CCTGTAATTCCAGTCTTTGTGCATTTGTCATCTGCCCTTAAAGGAATGATTTTCAACCTT

5650

5670

5690

TCTCCCTTCTCAAAATGCTTGCCTCATAATGCATAACTTCACTTTGACTCTGGTCTTGA

5710

5730

5750

AATTCCTAGTTTAATTGCGCTTGATGTTCTGCCTTATAAATGCACAATGATTTGTACTGT

5770

5790

5810

CTAATAAAAACAGTGTATACTTTGTATGTGTCGTGCATTCACTGGTCTTCATCCTGACAC

5830

5850

5870

AGTGGTTCGAGATCAAGTTGTACAGGCTGTGCATTTTAAGATACTAGTTTCAGTCTTTCA

5890

5910

5930

AAGCCAGCCAGGCTACACACAGAAAATGTTTACTCAATCATTCAAAAAGAGAAAAGGAG

5950

5970

5990

AGAAAGTAACTTTGTTTGGTAAAGCACCAGTACTCCAACCTTCCAGAAAGCCGATTATCT

6010

6030

6050

TCATTGCTTTTAATGTTCTATTCTGTGGCATATGGTTTCTGTACTTTGTTGTCAAAA

6070

6090

6110

TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACATAATGCATAAGCC

6130

6150

6170

ACACCAAAACAGACTCAATTTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

FIG. 27 J

6190	6210	6230
TGGCATTGAAACAAAAGACTTACTTACAAAGTTGCTGGCAGATGTATTTGATGGTTACTC		
6250	6270	6290
TTTTGTAATTCTTGTCCACTTGTAATTGTTTTTACTCTTTATACATACTTTTCAGACTG		
6310	6330	6350
CCTTTCTTTTGTAAATTTATGGACGGTTTATAAATGAATGACAAAGCTTTCCCCATTGTGT		
6370	6390	6410
CTTCAAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTTATTATTAAAGG		
6430	6450	6470
AAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGTGCATGTGCACAGTTAGTGTAAAATA		
6490		
TTTTCTAGAAATAAAATTTGTTATTTTAT		

FIG. 27 K

10 30 50
 GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAAGCCTGTGCACCTGGCCCTGTGC
 MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys

70 90 110
 ATGGGCACATGCTGGAGCCGCCCGTGGGCCCGCATCCTGCCACAGCCACAGGGCACCCC
 MetGlyThrCysTrpSerArgProTrpAlaProHisProAlaThrAlaThrGlyHisPro

130 150 170
 GGTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC
 GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer

190 210 230
 AGCAGGTTAGAGAAAAGGAGCGTCTTCTAGAGAGAAGCAGCGGGGCAGTACGCCGCC
 SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

250 270 290
 TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGCGCCTCGGTGGAC
 SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

310 330 350
 GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGGGAAACTGAGGCCACAGAATTGAGAA
 AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd

370 390 410
 TTTTGTCCATGATTACGCAGATGGTCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG

430 450 470
 CCTGAAGAAGACCTGTTTCCACGCCTTCCCCATGTGCCACGTTCTCCTCACCTATCCAG

490 510 530
 GAGTGAATCATCACCTTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA

550 570 590
 GCACTTGTTCTCTGGGTGAAGGACCCATACCCCCACTGGTTTTTGTAGATCGGCATTACGC

FIG. 28 A

610 630 650
 GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCCACCTG
 670 690 710
 GGGCTGAGTGTGACTGAGGCCCTGAATTTTTACTTCTATAAAATTAGTTCCAGATTAGTT
 730 750 770
 TACATTCCTAATTAGTTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA
 790 810 830
 CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTTCTAGAGAAGAGTAGAA
 850 870 890
 ACACAGCGGCAGAAACACAGCTCTGCACTTCCGAGGGCCTCCCACTCCTTCTGATGAGAC
 910 930 950
 TGCAGAGGAAGTCTGTTTGGCCAAGCATGCTATTAACACGTTTTCCTGCTTGTTTTGTTT
 970 990 1010
 TTTAACAGAGCAAACAGGTCTGTTTCTATTAAAATTTAAAAGCGTTAATATTTARCAGC
 1030 1050 1070
 ATTGTTTTATGTTGTATTTCATAACATAATAATATAACAATATATTAATTGTTAATATATA
 1090 1110 1130
 TTGTTAATAATATAATAATATAACATAAAATAAGTGATACTTATTTTCCATTTACAGTTG
 1150 1170 1190
 AGATATTTTCTTTAAAAGTAACGTAAATATTGATTCAATTCAAAGAATACATTCATTAA
 1210 1230 1250
 TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT
 1270 1290 1310

FIG. 28 B

Figure 6. The effect of the number of iterations on the accuracy of the proposed algorithm. The figure shows the accuracy of the proposed algorithm as a function of the number of iterations for different values of the parameter α . The x-axis represents the number of iterations (from 0 to 100), and the y-axis represents the accuracy (from 0.8 to 1.0). The legend indicates four cases: $\alpha = 0.1$ (blue line with circles), $\alpha = 0.2$ (orange line with triangles), $\alpha = 0.3$ (green line with squares), and $\alpha = 0.4$ (red line with diamonds). All curves show an increasing trend in accuracy as the number of iterations increases, eventually plateauing around 0.95 to 1.0.

1370

1430

1490

1550

1610

1650

AGTTATCTATTTTAAAAGTAAAAAAAACCTCGTGCCGAAGTC

FIG. 28 C